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(54) Title: POLYPEPTIDES OF G-COUPLED RECEPTOR PROTEINS, AND COMPOSITIONS AND METHODS THEREOF (57) Abstract Compounds, compositions and methods involving purified, isolated and/or synthetic G-protein coupled receptor (GPR) polypeptides that comprise fragments, derivatives and/or consensus peptides of transmembrane domains of G-coupled receptor proteins, wherein the GPR polypeptide has biological activity selected from binding of a GPR ligand to a GPR or modulating the binding of GPR a ligand to a GPR.		

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POLYPEPTIDES OF G-COUPLED RECEPTOR PROTEINS,
AND COMPOSITIONS AND METHODS THEREOF

FIELD OF THE INVENTION

The present invention relates to compounds,
5 compositions and methods involving synthetic, isolated and/or
recombinant G-protein coupled receptor polypeptides that
comprise fragments and/or consensus peptides of G-protein
coupled receptors.

BACKGROUND OF THE INVENTION

10 The membrane protein gene superfamily of G-protein
coupled receptors (GPRs) has been characterized as having seven
putative transmembrane domains. The domains are believed to
represent transmembrane α -helices connected by extracellular or
cytoplasmic loops. Of the 74 sequenced members of this
15 G-protein receptor superfamily, the shortest sequence of 324
amino acids represents the rat *mas* oncogene and the longest, of
744 amino acids, represents the human thyroid-stimulating
hormone (TSH) receptor. GPRs thus include a wide range of
biologically active receptors, such as hormone-, viral-, growth
20 factor- and neuroreceptors.

G-protein coupled receptors have been characterized as
including these seven conserved hydrophobic stretches of about
20-30 amino acids, connecting at least 8 divergent hydrophilic
loops. The G-protein family of coupled receptors includes
25 dopamine receptors which bind in a noncovalent but high affinity
manner to neuroleptic drugs used for treating psychotic and
neurological disorders. For example, the dopamine D₂ receptor
includes these transmembrane domains, two of which (TM III and
TM V; see below) have been implicated by site-selective
30 mutagenesis to demonstrate functional, association with D₂
ligands.

Transmembrane domains of G-protein coupled receptors
are designated TM1, TM2, TM3, TM4, TM5, TM6 and TM7. TM4, TM5,
TM6 and TM7 are the most highly conserved and are postulated to

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provide sequences which impart biological activity to GPRs. Most GPRs have single conserved cysteine residues in each of the first two extracellular loops which form disulfide bonds that are believed to stabilize functional protein structure. TM3 is also implicated in signal transduction.

Phosphorylation and lipidation (palmitoylation or farnesylation) of cysteine residues can influence signal transduction of some GPRs. Most GPRs contain potential phosphorylation sites (e.g., serine or threonine residues) within the third cytoplasmic loop and/or the carboxy terminus. For several GPRs, such as the β -adrenoreceptor, phosphorylation by protein kinase A and/or specific receptor kinases mediates receptor desensitization.

Non-limiting examples of GPRs include cAMP receptors, adenosine receptors, β -adrenergic receptors, muscarinic acetylcholine receptors, α -adrenergic receptors, serotonin receptors (5-HT), histamine H2 receptors, thrombin receptors, kinin receptors, follicle stimulating hormone receptors, opsins and rhodopsins, odorant receptors, cytomegalovirus receptor, etc. See e.g., Probst et al *DNA and Cell Biology* 11:1-20(1992), which is entirely incorporated herein by reference.

The ligand binding sites of GPRs are believed to comprise a hydrophilic socket formed by several GPR transmembrane domains, which socket is surrounded by hydrophobic residues of the GPRs. The hydrophilic side of each GPR transmembrane helix is postulated to face inward and form the polar ligand binding site. TM3 has been implicated in several GPRs as having a ligand binding site, such as including the TM3 aspartate residue. Additionally, TM5 serines, a TM6 asparagine and TM6 or TM7 phenylalanines or tyrosines are also implicated in ligand binding.

GPRs can be intracellularly coupled by heterotrimeric G-proteins to various intracellular enzymes, ion channels and transporters. See, e.g., Johnson et al *Endoc. Rev.* 10:317-331(1989) ; and Birnbaumer et al *Biochem. Biophys. Acta* 1031:163-224(1990) which references are incorporated entirely herein by reference. GPR agonist binding catalyzes the exchange

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of GTP for GDP on the α -subunit of the G-protein. Different G-protein α -subunits preferentially stimulate particular effectors to modulate various biological functions in a cell. Phosphorylation of cytoplasmic residues of GPRs has been
5 identified as an important mechanism for the regulation of G-protein coupling of some GPRs.

As a non-limiting example of a GPR ligand, dopamine (3,4-dihydroxyphenethylamine) is a critical neurotransmitter in the central nervous system (e.g., in the substantia nigra,
10 midbrain, and hypothalamus). Since the elucidation of the ascending mesolimbic and nigrostriatal pathways, these pathways have been found to be critical in the control of both motor initiation (nigrostriatal) behavior and affective (mesolimbic) behavior. The clinical efficacy of the major neuroleptic
15 antipsychotic medications has been found to correlate with the respective affinities of these agents for the dopamine D_2 receptor in the brain. A dopaminergic role in the symptomatology of the major psychoses has thus been hypothesized, although it is unclear if dopamine alone is
20 etiological, (see, e.g., Davis et al. *Am. J. Psych.* 148:1474-1476 (1991)). Nonetheless, this hypothesis has served as a stimulus for current research in this area.

One model for studying possible interactions of G-protein coupled receptors with their ligands has emerged from
25 site-directed mutagenesis and biochemical analysis of the β -adrenergic receptor, as well as from biophysical analysis of the interaction of retinal with opsin.

According to such a model, the binding of a GPR ligand to a G-protein coupled receptor involves multiple interactions
30 between functional groups on the GPR ligand and residues within the hydrophobic binding site of the receptor.

While a number of the amino acid residues in the dopamine D_2 receptor have been postulated to participate in D_2 ligand binding, based on results obtained from site-directed
35 mutagenesis studies and photoaffinity labeling studies performed on the β -adrenergic receptor, such studies have failed to specifically determine which residues are actually involved in

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binding in the D₂ system. Sibley et al. Soc. Neurosci. Abs. 17:36.10, 324.5, 324.6 (1991).

The clinical use of neuroleptics has provided a means for treating patients suffering from psychotic disorders.

- 5 Short-term use of neuroleptics is indicated in several types of psychotic disorders, e.g., acute psychotic episodes, regardless of type; exacerbations of schizophrenia; acute manic excitement while deferring use of lithium or awaiting onset of its effects; adjunctive therapy for major depression with prominent psychotic symptoms, or when an antidepressant or ECT alone is not successful; for agitation in delirium, dementia, or severe mental retardation while seeking to identify and treat the primary basis of the problem; in certain chronic, degenerative, or idiopathic neuropsychiatric disorders with dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome; or for ballism or hemiballism; childhood psychoses or apparently allied conditions marked by severe agitation or aggressive behavior; miscellaneous medical indications, notably nausea and vomiting, or intractable hiccups.

Additionally, continuous long-term use of neuroleptics is indicated in many psychotic disorders, such as (for more than six months) (i) primary indications such as Schizophrenia, Paranoia^{a,b}, Childhood psychoses, some degenerative or idiopathic neuropsychiatric disorders (notably, Huntington's disease and Gilles de la Tourette's syndrome); (ii) secondary indications such as extremely unstable manic-depressive or other episodic psychoses (unusual), otherwise unmanageable behavior symptoms in dementia, amnesia, or other brain syndromes; and (iii) questionable indications such as chronic characterological disorders with schizoid, "borderline," or neurotic characteristics; substance abuse; or antisocial behavior, recurrent mood disorders. See, e.g., Baldessarini, *Chemotherapy in Psychiatry*, Revised and Enlarged Edition, Harvard University Press, Cambridge, MA, (1985), the contents of which is entirely incorporated herein by reference.

Neuroleptics are also referred to as neuroplegics, psychoplegics, psycholeptics, antipsychotics and major

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tranquilizers, but are sometimes distinguished from non-neuroleptic anti-psychotics. Neuroleptics have recently been characterized as an agent that produces sedative or tranquilizing effects, and which also produces motor side effects, such as catalepsy or extrapyramidal symptomatology. Nonlimiting representative examples of neuroleptics include phenothiazine derivatives (e.g., chlorpromazine); thioxanthine derivatives (e.g., thiothixene); butyrophenone derivatives (e.g., haloperidol); dihydroindolone (e.g., molindone); dibenzoxazepine derivatives (e.g., loxapine); and "atypical" neuroleptics (e.g., sulpiride, remoxipiride pimozone and clozapine). See Berstein *Clinical Pharmacology* Littleton, Mass.:PSG Publishing (1978); Usdin et al *Clinical Pharmacology in Psychiatry* New York:Elsevier North-Holland (1981); and Baldessarini, *supra*, (1985); and , which references are herein entirely incorporated by reference.

The term "atypical neuroleptics" has been used to describe antipsychotic neuroleptics that produce few or no extrapyramidal side effects and which do not cause catalepsy in animals (See, e.g., Picket et al, *Arch. Gen. Psychiatry* 49:345 (May 1992). Alternatively, atypical neuroleptics, such as clozapine, have been described as those neuroleptics which have a higher affinity for D₄ and D₁ sites than for D₂ sites (See, e.g., Davis et al *Amer. J. Psych.* 148:1474, 1476 (November 1991)).

The long term use of all known anti-psychotics, such as neuroleptics or non-neuroleptic antipsychotics, has resulted in serious side effects, as present in Table I, such as persistent and poorly reversible motoric dysfunctions (e.g., tardive dyskinesia) in a significant number of patients. These side effects are especially prevalent in geriatric populations, and adequate pharmacological treatment of these debilitating motoric dysfunctions is not currently available. This problem has severely limited the long-term, clinical administration of these agents.

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TABLE I
Neurological Side Effects of
Neuroleptic-Antipsychotic Drugs

Reaction	Features	Period of maximum risk	Proposed mechanism	Treatment
Acute dystonia	Spasm of muscles of tongue, face, neck, back; may mimic seizures; not hysterical	1-5 days	Dopamine excess? Acetylcholine excess?	Antiparkinsonism agents are diagnostic and curative (i.m. or i.v., then p.o.)
Parkinsonism	Bradykinesia, rigidity, variable tremor, mask-facies, shuffling gait	5-30 days (rarely persists)	Dopamine blockade	Antiparkinsonism agents (p.o); dopamine agonists risky?
Akathisia	Motor restlessness; patient may experience anxiety or agitation	5-60 days (commonly persists)	Unknown	Reduce dose or change drug low doses of propranolol; ^a antiparkinsonism agents or or benzodiazepines may help
Tardive dyskinesia	Oral-facial dyskinesia; choreo-athetosis, sometimes irreversible, rarely progressive	6-24 months (worse on withdrawal)	Dopamine excess?	Prevention best; treatment unsatisfactory; slow spontaneous remission
"Rabbit" syndrome	Perioral tremor (late parkinsonism variant?); usually reversible	Months or years	Unknown	Antiparkinsonism agents; reduce dose of neuroleptic
Malignant syndrome	Catatonia, stupor, fever, unstable pulse and blood pressure; myoglobinemia; can be fatal	Weeks	Unknown	Stop neuroleptic; antiparkinsonism agents usually fail; bromocriptine often helps; dantrolene variable; general supportive care crucial

a. There may be an increased risk of hypotension on interacting high doses of propranolol with some antipsychotic agents; clonidine may also be effective at doses of 0.2-0.8 mg/day, but carries a high risk of hypotension (Zubenko et al., *Psychiatry Res.* 11:143, 1984).

In addition, clozapine, although apparently capable of producing less motor side effects, can cause irreversible, potentially fatal agranulocytosis in a minority of patients administered the drug. Such serious side effects limit the use of

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clozapine to patients who are resistant to treatment with other neuroleptics.

Antipsychotics have a variety of significant pharmacological effects, e.g., as presented in the following
5 Tables II and III.

Table II
Comparative Pharmacology of Neuroleptics

Alkaloid Pharmacologic Actions	Phenothiazine Derivative Chlorpromazine	Thioxanthene Derivative Thiothixene	Butyrophenone Derivative Haloperidol
Antipsychotic	Yes + +	Yes + +	Yes + + + +
Antiemetic	Yes + + +	Not tested	Yes + + +
Hypothermia	Yes +	Yes +	No
Hypotension	Yes + +	Yes + + +	+
Parkinsonism	Yes + +	Yes +	Yes + + + +
Antiadrenergic	Yes + +	Yes + + +	+
Anticholinergic	Yes +	Yes +	Negligible
Antihistaminic	Yes +	Negligible	Negligible
Releases NE, DA	No	No	No
Blocks DA	Yes + +	Yes +	Yes + + + +
Blocks NE	Yes + +	Yes + + +	Yes +
Central sympathetic suppressant	Yes + +	Yes +	Yes + + +

Chlorpromazine, thiothixene, and haloperidol decrease the functional availability of dopamine (DA) and norepinephrine (NE) by blocking the dopamine receptor sites in the basal ganglia and norepinephrine receptor sites in thalamic and hypothalamic areas. Reserpine simply reduces the concentrations of norepinephrine and dopamine in these areas. Both of these actions result in suppression of central sympathetic activity.
+ + + + + indicates from very weak to very strong effects.

Table III
Comparative Pharmacology of Antipsychotics

Extrapyramidal Drug	Sedation	Adrenergic Blockage	Reaction
Chlorpromazine	High	Moderate to high	Moderate
Chlorprothixene	High	High	Low to moderate
Haloperidol	Low	Low	High
Molindone	Moderate	Moderate	Moderate to high
Loxapine	High	Low to moderate	High

See Ebadi, PHARMACOLOGY, Little, Brown and Co., Boston, 61-65 (1985); Cattabeni et al *Adv. Biochem. Psychopharmacology* 24:275 (1980). Baldessarini, *supra*, which references are herein incorporated entirely by reference.

5 However, despite the fact that thousands of neuroleptic- or antipsychotic-type compounds have been synthesized and reported in the literature, such compounds which lack serious side effects and which have sufficient pharmacological activity, have not been disclosed.

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Alternative to dopamine receptor GPRs, as presented above, other neuroreceptor GPRs are involved in neurological pathologies, and drugs such as neuroreceptor GPR binding agents, presently used for treating these pathologies, also suffer from similar side effects as those of neuroleptics, as presented above.

Other GPRs are also involved in receptor-related pathologies, such as hormone related GPRs involved in endocrine related pathologies.

Accordingly, there is a need to provide G-protein coupled receptor binding agents, including neuroreceptor and endocrine receptor GPRs, which do not produce such deleterious and debilitating side effects as those produced by known agents, such as neuroleptics, which can be used for therapy or diagnosis of GPR related pathologies.

Citation of documents herein is not intended as an admission that any of the documents cited herein is pertinent prior art, or an admission that the cited documents are considered material to the patentability of the claims of the present application. All statements as to the date or representations as to the contents of these documents are based on the information available to the applicant and does not constitute any admission as to the correctness of the dates or contents of these documents.

SUMMARY OF THE INVENTION

It is therefore an object of the present invention to overcome one or more deficiencies found in the related art.

It is another object of the present invention to provide non-naturally occurring synthetic, isolated and/or recombinant GPR polypeptides which are fragments, consensus fragments and/or sequences having conservative amino acid substitutions, of at least one transmembrane domain of at least one G-protein coupled receptor, which polypeptides have been discovered to have receptor-like functional binding sites of neuroreceptor and endocrine GPRs, such that GPR polypeptides of the present invention may bind GPR ligands, or which may also modulate, quantitatively or qualitatively, GPR ligand binding to GPRs.

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It is still another object of the present invention to provide GPR polypeptides and compositions that have only partially helical structures, in contrast to known characterized transmembrane domains of GPRs, such as, but not limited to, GPR
5 transmembrane domains I-VII.

It is yet another object of the present invention to provide synthetic or recombinant GPR polypeptides, conservative substitution derivatives thereof, antibodies, anti-idiotypic antibodies, compositions and methods that can be used as potential
10 modulators of G-protein coupled receptor function, by binding to GPR ligands or modulate GPR ligand binding, due to their expected biological properties, which may be used in diagnostic, therapeutic and/or research applications.

It is a further object of the present invention is to
15 provide synthetic, isolated or recombinant polypeptides which are designed to inhibit or mimic various GPRs or fragments thereof, as receptor types and subtypes.

According to one aspect of the present invention, a synthetic or recombinant GPR polypeptide is provided that
20 comprises a GPR amino acid sequence of, e.g., at least 5, 10, 15 or 20 amino acids, substantially corresponding to at least one transmembrane domain, or fragment and/or consensus peptide thereof, of a G-protein coupled receptor, wherein at least 20 amino acids are preferred. In a preferred embodiment, the
25 polypeptide is (a) chemically synthesized and/or (b) obtained from a recombinant host cell or organism which expresses a recombinant nucleic acid encoding a GPR polypeptide, as defined herein.

In another preferred embodiment, the transmembrane domain is selected from at least one of TM1, TM2, TM3, TM4, TM5, TM6 or
30 TM7, corresponding to transmembrane domains I, II, III, IV, V, VI and VII, respectively, of a GPR. In another preferred embodiment, the transmembrane domain is a dopamine receptor transmembrane domain selected from the group consisting of at least one of a D₁, D₂, D₃, D₄ and D₅ dopamine receptor transmembrane domain. The
35 transmembrane domain, e.g., may be selected from at least one of D₂ receptor transmembrane domains III or V. In still another preferred embodiment, the GPR polypeptide amino acid sequence

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substantially corresponding to an amino acid sequence contained in at least one of Fig. 2 (SEQ ID NO:2), Fig. 3 (SEQ ID NO:3) or Fig. 5 (SEQ ID NO:5).

In another aspect of the present invention, a GPR composition is provided, comprising a GPR polypeptide, or a pharmaceutically acceptable ester, ether, sulfate, carbonate, malate, glucuronide or salt thereof, the composition further comprising a pharmaceutically acceptable carrier and/or diluent.

In still another aspect of the present invention, a method is provided for treating a subject suffering from a disease state involving a qualitative or quantitative pathological abnormality of a GPR protein or a biological molecule functionally associated therewith. Such biological molecule may be a membrane cytoplasmic protein, lipid, carbohydrate, saccharide, nucleoside or nucleotide mono-, di-, or tri-phosphate, an enzyme, a co-factor, a nucleic acid, a neurotransmitter, an ion, a carrier, a cell receptor, or any combination thereof.

In a preferred embodiment, the GPR protein is a dopamine receptor and the abnormality involves a dopamine related pathology, wherein the method comprises administering an effective dopamine receptor modulating amount of a GPR polypeptide of the present invention. In another preferred embodiment, the transmembrane domain is a D₂ dopamine receptor domain and the disease state is a psychiatric disorder, such as schizophrenia or schiz affective disorder (see American Psychiatric Association, Revised Manual of Diagnostic and Statistical Criteria for Psychiatric Disorders (DSM-III-R), American Psychiatric Assoc. Press, Washington, DC (1989)).

In another preferred embodiment, the GPR composition is administered as a pharmaceutical composition to provide a GPR polypeptide in an amount ranging from about 0.01 µg to 100 mg/kg, and also preferably, about 10 µg to 10 mg/kg. In another preferred embodiment, the administering is by oral, intravenous, intramuscular, parenteral or topical administration, including mucosal administration to the nasal mucosa or the oral mucosa, by aerosol, nebulizer or drop administration as non-limiting examples.

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Other objects of the invention will be apparent to skilled practitioners from the following detailed description and examples relating to the present invention.

5

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is the amino acid sequence of a control peptide (SEQ ID NO:1), which is hydrophobic in its properties, but does not correspond to a known GPR transmembrane domain.

10 Fig. 2 represents the amino acid sequence of a GPR transmembrane polypeptide, polypeptide II (SEQ ID NO:2), which corresponds to a portion of the dopamine D₂ receptor transmembrane segment III.

15 Fig. 3 represents the amino acid sequence of a transmembrane polypeptide, polypeptide III (SEQ ID NO:3), corresponding to a consensus peptide of the dopamine D₂ receptor transmembrane domains I-VII.

Fig. 4 represents the amino acid sequence of a consensus sequence of transmembrane domains that is shortened to be less than the length required to span a lipid bilayer.

20 Fig. 5 represents a consensus amino acid sequence of transmembrane domain as a consensus peptide between dopamine receptors D₁ and D₂.

25 Fig. 6 is a representation of a circular dichroism spectrum of a solution of the consensus polypeptide III (SEQ ID NO:3) of Fig. 3.

Fig. 7 is a graphical representation of radioligand binding assay data comparing control polypeptide II (SEQ ID NO:1) of Fig. 1, labeled as "II" and consensus polypeptide I (SEQ ID NO:3) of Fig. 3, labeled as "I".

30 Fig. 8A-G are a comparison listing of amino acid sequences of transmembrane domains and adjacent amino acid sequences of representative GPRs (SEQ ID NOS:6-79).

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention relates to G-protein coupled receptor (GPR) polypeptides which can be used to mimic naturally occurring or isolated GPRs, or to modulate the binding of GPR ligands to GPRs, such as inhibition or enhancement of binding. GPR polypeptides of the present invention can include GPR transmembrane domain fragments and/or consensus peptides thereof, of at least 4-10 amino acids in length, and/or corresponding sequences having conservative amino acid substitutions as "substitution peptides", wherein the GPR polypeptide binds a GPR ligand or modulates the binding of a GPR ligand to a GPR *in vitro*, *in vivo* or *in situ*.

GPR polypeptides of the present invention can be synthesized or recombinantly produced, or optionally purified, to provide commercially useful amounts of GPR polypeptides for use in therapeutic, diagnostic or research applications, according to known method steps, see, e.g., Ausubel et al, eds. Current Protocols in Molecular Biology, Wiley Interscience, N.Y., (1987, 1992); and Sambrook et al, Molecular Cloning, A Laboratory Manual, 2nd edition, Vols. 1-3, Cold Spring Harbor Press, (1989), which references are herein entirely incorporated by reference.

Additionally, GPR polypeptides according to the present invention can be used to generate polyclonal and/or monoclonal antibodies, anti-idiotypic antibodies thereto, or fragments thereof, which may be used for diagnostic and/or therapeutic applications, according to known method steps, see, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Press (1988), which is herein entirely incorporated by reference.

GPR polypeptides, anti-GPR antibodies or anti-idiotypic antibodies (or fragments thereof) to GPR polypeptides have been unexpectedly discovered to quantitatively or qualitatively modulate G-protein coupled receptors, such that binding of GPR polypeptides or anti-idiotypic antibodies (or fragments thereof) to G-protein coupled receptor ligands may be used for diagnostic research or therapeutic applications of the present invention. Such GPR polypeptides, antibodies or anti-idiotypic antibodies of the present invention may therefore be used as modulators of

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G-protein coupled receptors, such as neuroreceptors or endocrine receptors, as non-limiting examples.

Binding of such GPR polypeptides, (including GPR fragments, consensus peptides, substitution derivatives and anti-
5 idiotype antibody fragments) of the present invention may be used to treat symptoms of, and provide diagnosis and treatment for, pathologies related to GPRs. Such pathologies have been found to correlate with symptoms occurring in neurological, viral or endocrine pathologies. D₂ receptor-related psychotic disorders,
10 including schizophrenia, now treated with neuroleptics, is a non-limiting example thereof.

The use of synthetic or recombinant GPR polypeptides of the present invention can be preferable to the use of known drugs that bind G-protein coupled receptors, such as neuroleptics that
15 bind or inhibit the biological effect of binding to neuroreceptors as a non-limiting example. Such polypeptides are expected to have significantly less side effects than presently used drugs presently used for inhibiting such receptor binding including neuroleptics, as they would structurally mimic naturally occurring
20 GPRs and/or modulate ligand binding. Thus, GPR polypeptides are expected to have reduced side effects attributable to known foreign compound drugs, with less immunogenicity, and reduced potential for motoric side effects (e.g., extrapyramidal symptoms and/or tardive dyskinesia).

25 The present invention is also related to the production, by chemical synthesis or recombinant DNA technology, of GPR polypeptides, preferably as small as possible while still retaining sufficiently high affinity or interaction with G-protein coupled receptors to modulate, such as to inhibit or to enhance,
30 binding to such receptors by GPR ligands.

GPR polypeptides of the present invention may include 5-
10 to 50-150 amino acid fragments, consensus sequences or substitution sequences of GPRs, e.g., as presented in Fig. 8A-G (SEQ ID NOS:6-79) including, but not limited to, multiple dopamine
35 receptors, cAMP receptors, adenosine receptors, β -adrenergic receptors, muscarinic acetylcholine receptors, α -adrenergic receptors, serotonin receptors (5-HT), histamine H₂ receptors,

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thrombin receptors, kinin receptors, follicle stimulating hormone receptors, opsins and rhodopsins, odorant receptors, cytomegalovirus GPRs, adenosine A2 receptors, dopamine receptor, histamine H2 receptors, octopamine receptors, N-formyl receptors, anaphylatoxin receptors, thromboxane receptors, IL-8 receptors, platelet activating factor receptors, endothelin receptors, bombesin gastrin releasing peptide receptor, neuromedin B preferring bombesin receptors, vasoactive intestinal peptides, neurotensin receptors, bradykinin receptors, thyrotropin-releasing hormone receptors, substance P receptors, neuromedin K receptors, adrenal angiotensin II type I receptors, *mas* oncogene (angiotensin) receptors, lutropin-choriogonadotropin receptors, thyrotropin receptors, follicle stimulating hormone receptors, cannabinoid receptors, glucocorticoid-induced receptors, endothelial cell GPRs, testis GPRs, and thoracic aorta GPRs, and homologs thereof having a homology of at least 80% with at least one of transmembrane domains 1-7, as described herein. See, e.g., Probst et al *DNA and Cell Biology* 11:1-20(1992), which is entirely incorporated herein by reference.

Accordingly, a "G-protein coupled receptor polypeptide" or "GPR polypeptide" of the present invention includes polypeptides having a "GPR amino acid sequence" which substantially corresponds to at least one 10 to 50 amino acid fragment and/or consensus sequence of a known GPR or group of GPRs, wherein the GPR polypeptide has homology of at least 80%, such as 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% homology, while maintaining GPR modulating activity, wherein a GPR polypeptide of the present invention is not naturally occurring or is naturally occurring but is in a purified or isolated form which does not occur in nature. Preferably, a GPR polypeptide of the present invention substantially corresponds to a transmembrane domain of a GPR or group of GPRs as a consensus sequence.

Also preferred are GPR polypeptides wherein the GPR amino acid sequence is 4-10 to 50 amino acids in length, such as 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39,

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40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140 or 150 amino acids, or any range therein.

An amino acid or nucleic acid sequence of a GPR polypeptide of the present invention is said to "substantially
5 correspond" to another amino acid or nucleic acid sequence, respectively, if the sequence of amino acids or nucleic acid in both molecules provides polypeptides having biological activity that is substantially similar, qualitatively or quantitatively, to the corresponding fragment of at least one GPR transmembrane
10 domain, or which may be synergistic when two or more transmembrane domains, consensus sequences or homologs thereof are present.

Additionally or alternatively, such "substantially corresponding" sequences of GPR polypeptides include conservative amino acid or nucleotide substitutions, or degenerate nucleotide
15 codon substitutions wherein individual amino acid or nucleotide substitutions are well known in the art.

Alternatively or additionally, substantially corresponding refers to GPR polypeptides having amino acid sequences having at least 80% homology or identity to an amino
20 acid sequence of SEQ ID NO:1, such as 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% homology or identity.

Accordingly, GPR polypeptides of the present invention, or nucleic acid encoding therefor, include a finite set of
25 substantially corresponding sequences as substitution peptides or polynucleotides which can be routinely obtained by one of ordinary skill in the art, without undue experimentation, based on the teachings and guidance presented herein. For a detailed description of protein chemistry and structure, see Schulz, G.E.
30 et al., *Principles of Protein Structure*, Springer-Verlag, New York, 1978, and Creighton, T.E., *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, 1983, which are hereby incorporated by reference. For a presentation of nucleotide sequence substitutions, such as codon preferences, see
35 Ausubel et al, *supra*, at §§ A.1.1-A.1.24, and Sambrook et al, *supra*, at Appendices C and D.

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Conservative substitutions of a GPR polypeptide of the present invention includes a variant wherein at least one amino acid residue in the polypeptide has been conservatively replaced by a different amino acid. Such substitutions preferably are made in accordance with the following list as presented in Table IV, which substitutions may be determined by routine experimentation to provide modified structural and functional properties of a synthesized polypeptide molecule, while maintaining the receptor binding, inhibiting or mimicking biological activity, as determined by known GPR receptor activity assays.

Table IV

<u>Original Residue</u>	<u>Exemplary Substitution</u>
Ala	Gly;Ser
Arg	Lys
Asn	Gln;His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Ala;Pro
His	Asn;Gln
Ile	Leu;Val
Leu	Ile;Val
Lys	Arg;Gln;Glu
Met	Leu;Tyr;Ile
Phe	Met;Leu;Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp;Phe
Val	Ile;Leu

Alternatively, another group of substitutions of GPR polypeptides of the present invention are those in which at least one amino acid residue in the protein molecule has been removed and a different residue inserted in its place according to the following Table V. The types of substitutions which may be made in the protein or peptide molecule of the present invention may be based on analysis of the frequencies of amino acid changes between a homologous protein of different species, such as those presented in Table 1-2 of Schulz et al., supra and Figs. 3-9 of Creighton, supra.

Based on such an analysis, alternative conservative substitutions are defined herein as exchanges within one of the following five groups:

TABLE V

1. Small aliphatic, nonpolar or slightly polar residues: Ala, Ser, Thr (Pro, Gly);
2. Polar, negatively charged residues and their amides: Asp, Asn, Glu, Gln;
3. Polar, positively charged residues: His, Arg, Lys;
4. Large aliphatic, nonpolar residues: Met, Leu, Ile, Val (Cys); and
5. Large aromatic residues: Phe, Tyr, Trp.

The three amino acid residues in parentheses above have special roles in protein architecture. Gly is the only residue lacking any side chain and thus imparts flexibility to the chain. This however tends to promote the formation of secondary structure other than α -helical. Pro, because of its unusual geometry, tightly constrains the chain. It generally tends to promote β -turn-like structures, although in some cases Cys can be capable of participating in disulfide bond formation which is important in protein folding. Note the Schulz et al. would merge Groups 1 and 2, above. Note also that Tyr, because of its hydrogen bonding potential, has significant kinship with Ser, and Thr, etc.

Conservative amino acid substitutions according to the present invention, e.g., as presented above, are known in the art and would be expected to maintain biological and structural properties of the polypeptide after amino acid substitution. Most deletions and insertions, and substitutions according to the present invention are those which do not produce radical changes in the characteristics of the protein or peptide molecule. "Characteristics" is defined in a non-inclusive manner to define both changes in secondary structure, e.g. α -helix or β -sheet, as well as changes in physiological activity, e.g. in receptor binding assays.

However, when the exact effect of the substitution, deletion, or insertion is to be confirmed one skilled in the art will appreciate that the effect of the substitution or substitutions will be evaluated by routine screening assays, either immunoassays or bioassays to confirm biological activity, such as receptor binding or modulation of ligand binding to the corresponding GPR. See, e.g., Maranges et al., eds., for example, a substituted polypeptide

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typically is made by site-specific mutagenesis of the peptide molecule-encoding nucleic acid, expression of the mutant nucleic acid in recombinant cell culture, and, optionally, purification from the cell culture, for example, by immunoaffinity chromatography using a
5 specific antibody on a chemically derivatized column or immobilized membranes or hollow fibers (to absorb the mutant by binding to at least one epitope).

A preferred use of this invention is the production, by chemical or recombinant DNA technology, of GPR polypeptides,
10 preferably as small as possible while still retaining sufficiently high affinity for binding to, or association with, GPRs. By production of GPR polypeptides including smaller fragments or variants of such transmembrane domains, one skilled in the art, using known binding and inhibition assays, can readily identify the GPR
15 polypeptides capable of binding minimizing or modulating G-protein coupled receptors using known methods. Non-limiting examples of fragments of GPRs to be used as GPR polypeptides or as a basis for consensus sequences thereof for GPR polypeptides, are presented in Figs. 2-5 and Fig. 8A-G, wherein fragments or consensus sequences of
20 10 to 50 amino acids of at least one sequence of Figs. 2-5 or corresponding to at least one transmembrane domain or domains 1-7 listed in Fig. 8A-G (SEQ ID NOS:6-79) are encompassed by the present invention, such as at least one transmembrane domain of one or more GPRs, such as a cAMP receptor (1), adenosine receptors (2-3);
25 muscarinic acetylcholine receptors (4-8); human adrenergic receptors (9-11, 14-16, 19-25, 28); adrenergic receptors (9-28); human thrombin receptor (31); endothelin receptors (35-36), bombesin receptors (37-38), endocrine receptors (48-50), rhodopsin (51), opsins (52-54), odorant receptors (55-64), and cytomegalovirus GPRs (72-54), as non-
30 limiting examples, wherein ("#") refers to the listed sequences in Fig. 8A-G.

Accordingly, GPR polypeptides may include consensus sequences and/or fragments of at least one of transmembrane domain 1-7 of one or more GPRs as presented in Figs. 2-5 (SEQ ID NO:2-5) or
35 Fig. 8A-G. (SEQ ID NOS:6-79) or homologs thereof, which GPR polypeptides do not occur naturally, and/or which are provided in an isolated and/or purified form not found in nature.

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Consensus peptides of GPR polypeptides of the present invention may include peptides which are distinct from known GPR sequences in critical structural features, but which are derived from consensus sequences of homologous GPR transmembrane domains 1-7, e.g., as presented in Fig. 8A-G (SEQ ID NOS:6-79). Such consensus peptides may be derived by molecular modeling, optionally combined with hydrophobicity analysis and/or fitting to model helices, as non-limiting examples. Such modeling can be accomplished according to known method steps using known modeling algorithms, such as, but not limited to, ECEPP, INSIGHT, DISCOVER, CHEM-DRAW, AMBER, FRODO and CHEM-X. Such algorithms compare transmembrane domains between related G-protein coupled receptors, determine probable energy-minimized structures and define alternative consensus polypeptide fragments.

Such consensus peptides or fragments of GPRs may then be synthesized or produced recombinantly, in order to provide GPR polypeptides according to the present invention which mimic, modulate or inhibit binding of ligands to G-protein coupled receptors. GPR ligands, in the context of the present invention, refer to biological molecules that bind GPRs *in vitro*, *in situ* or *in vivo*, and may include hormones, neurotransmitters, viruses or receptor binding domains, thereof, opsins, rhodopsins, nucleosides, nucleotides, coagulation cascade factors, odorants or pheromones, toxins, colony stimulating factors, platelet activating factors, neuroactive peptides, neurohumors, or any biologically active compounds, such as drugs or synthetic or naturally occurring compounds.

The following non-limiting examples of consensus peptides of GPRs of the present invention are provided by way of guidance and not by way of limitation. In GPR polypeptides of the present invention, one or more, preferably 4-10, Asp and/or Lys residues may additionally be incorporated at the carboxy and/or amino terminal ends in order to provide expected helix forming effects of the helix dipole effect, e.g., as described in Baldwin et al *Biochem.* 28:2130 (1989); Baldwin et al *Proc. Nat'l Acad. Sci. USA* 84:8898 (1987); and Baldwin et al *Proc. Nat'l Acad. Sci. USA* 86:5286 (1989), which references are entirely incorporated herein by reference.

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As a non-limiting example of GPR polypeptide of the present invention, dopamine receptor transmembrane fragments of D₂ transmembrane domain (e.g., domain III) as presented in Fig. 2 (SEQ ID NO:2) or a consensus sequence as presented in Fig. 3 (SEQ ID NO:3), e.g., of D₂ domains I-VII. Additionally or alternatively a consensus sequence may include less than 20 amino acids, such as 15 amino acids corresponding to a transmembrane domain, such as a D₂ receptor domain, as presented in Fig. 4 (SEQ ID NO:4) as polypeptide IV, which is smaller than the length required by spanning an average lipid bilayer of a cell membrane.

However, in the context of the present invention, GPR polypeptides of greater than 15 -20 amino acids are preferred such that the GPR polypeptides are able to span the lipid bilayer.

Another non-limiting example of a GPR polypeptide using dopamine receptor transmembrane domains is a consensus sequence of two or more GPR receptors, such as the dopamine D₁ and D₂ receptors. A non-limiting example of such a consensus GPR polypeptide is presented in Fig. 5 (SEQ ID NO:5).

Additionally, modified amino acids or chemical derivatives of amino acids of consensus or fragments of GPRs proteins, according to the present invention may be provided, which polypeptides contain additional chemical moieties or modified amino acids not normally a part of the protein. Covalent modifications of the peptide are thus included within the scope of the present invention. Such modifications may be introduced into a GPR polypeptide by reacting targeted amino acid residues of the polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or terminal residues. The following examples of chemical derivatives are provided by way of illustration and not by way of limitation.

Aromatic amino acids may be replaced with D- or L-naphthylalanine, D- or L-Phenylglycine, D- or L-2-thieneylalanine, D- or L-1-, 2-, 3- or 4-pyreneylalanine, D- or L-3-thieneylalanine, D- or L-(2-pyridinyl)-alanine, D- or L-(3-pyridinyl)-alanine, D- or L-(2-pyrazinyl)-alanine, D- or L-(4-isopropyl)-phenylglycine, D-(trifluoromethyl)-phenylglycine, D-(trifluoromethyl)-phenylalanine, D-p-fluorophenylalanine, D- or L-p-biphenylphenylalanine, D- or

L-p-methoxybiphenylphenylalanine, D- or L-2-indole(alkyl)alanines, and D- or L-alkylalanines where alkyl may be substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, non-acidic amino acids, of C1-C20.

Acidic amino acids can be substituted with non-carboxylate amino acids while maintaining a negative charge, and derivatives or analogs thereof, such as the non-limiting examples of (phosphono)-alanine, glycine, leucine, isoleucine, threonine, or serine; or sulfated (e.g., $-SO_3H$) threonine, serine, tyrosine.

Other substitutions may include unnatural hydroxylated amino acids may be made by combining "alkyl" (as defined and exemplified herein) with any natural amino acid. Basic amino acids may be substituted with alkyl groups at any position of the naturally occurring amino acids lysine, arginine, ornithine, citrulline, or (guanidino)-acetic acid, or other (guanidino)alkyl-acetic acids, where "alkyl" is defined as above. Nitrile derivatives (e.g., containing the CN-moiety in place of COOH) may also be substituted for asparagine or glutamine, and methionine sulfoxide may be substituted for methionine. Methods of preparation of such peptide derivatives are well known to one skilled in the art.

In addition, any amide linkage in any of the GPR polypeptides can be replaced by a ketomethylene moiety, e.g. $(-C(=O)-CH_2-)$ for $(-C(=O)-NH-)$. Such derivatives are expected to have the property of increased stability to degradation by enzymes, and therefore possess advantages for the formulation of compounds which may have increased *in vivo* half lives, as administered by oral, intravenous, intramuscular, intraperitoneal, topical, rectal, intraocular, or other routes.

In addition, any amino acid representing a component of the said peptides can be replaced by the same amino acid but of the opposite chirality. Thus, any amino acid naturally occurring in the L-configuration (which may also be referred to as the R or S, depending upon the structure of the chemical entity) may be replaced with an amino acid of the same chemical structural type, but of the opposite chirality, generally referred to as the D- amino acid but which can additionally be referred to as the R- or the S-, depending

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upon its composition and chemical configuration. Such derivatives have the property of greatly increased stability to degradation by enzymes, and therefore are advantageous in the formulation of compounds which may have longer *in vivo* half lives, when
5 administered by oral, intravenous, intramuscular, intraperitoneal, topical, rectal, intraocular, or other routes.

Additional amino acid modifications of amino acids of GPR polypeptides of to the present invention may include the following: Cysteiny l residues may be reacted with alpha-haloacetates (and
10 corresponding amines), such as 2-chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteiny l residues may also be derivatized by reaction with compounds such as bromotrifluoroacetone, alpha-bromo-
beta-(5-imidozoyl)propionic acid, chloroacetyl phosphate,
15 N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

Histidyl residues may be derivatized by reaction with compounds such as diethylprocarbonate e.g., at pH 5.5-7.0 because
20 this agent is relatively specific for the histidyl side chain, and para-bromophenacyl bromide may also be used; e.g., where the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0.

Lysiny l and amino terminal residues may be reacted with compounds such as succinic or other carboxylic acid anhydrides.
25 Derivatization with these agents is expected to have the effect of reversing the charge of the lysiny l residues. Other suitable reagents for derivatizing alpha-amino-containing residues include compounds such as imidoesters/e.g., as methyl picolinimide; pyridoxal phosphate; pyridoxal; chloroborohydride;
30 trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginy l residues may be modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin according to
35 known method steps. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these

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reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

The specific modification of tyrosyl residues per se is well-known, such as for introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. N-acetylimidizol and tetranitromethane may be used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

Carboxyl side groups (aspartyl or glutamyl) may be selectively modified by reaction with carbodiimides (R' N-C-N-R') such as 1-cyclohexyl-3-(2-morpholinyl- (4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4- dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues may be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

Glutaminyl and asparaginyl residues may be frequently deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues may be deamidated under mildly acidic conditions. Either form of these residues falls within the scope of the present invention.

Derivatization with bifunctional agents is useful for cross-linking the peptide to a water-insoluble support matrix or to other macromolecular carriers, according to known method steps. Commonly used cross-linking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithiol]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Patent Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 (which are herein incorporated entirely by reference), may be employed for protein immobilization.

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Other modifications of GPR polypeptides of the present invention may include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains (T.E. Creighton, *Proteins: Structure and Molecule Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)), acetylation of the N-terminal amine, methylation of main chain amide residues (or substitution with N-methyl amino acids) and, in some instances, amidation of the C-terminal carboxyl groups, according to known method steps.

Such derivatized moieties may improve the solubility, absorption, permeability across the blood brain barrier biological half life, and the like. Such moieties or modifications of GPR polypeptides may alternatively eliminate or attenuate any possible undesirable side effect of the protein and the like. Moieties capable of mediating such effects are disclosed for example, in *Remington's Pharmaceutical Sciences*, 16th ed., Mack Publishing Co., Easton, PA (1980).

Such chemical derivatives of GPR polypeptides also may provide attachment to solid supports, including but not limited to, agarose, cellulose, hollow fibers, or other polymeric carbohydrates such as agarose, cellulose, such as for purification, generation of antibodies or cloning; or to provide altered physical properties, such as resistance to enzymatic degradation or increased binding affinity or modulation for GPRs, which is desired for therapeutic compositions comprising GPR polypeptides, antibodies thereto or fragments thereof. Such peptide derivatives are well-known in the art, as well as method steps for making such derivatives using carbodiimides active esters of N-hydroxy succinimide, or mixed anhydrides, as non-limiting examples.

Variation upon consensus peptide sequences of GPR polypeptide of the present invention may also include: the addition of one, two, three, four, or five lysine, arginine or other basic residues added to the -COOH terminal end of the peptide; and/or one, two, three, four, or five glutamate or aspartate or other acidic residues added to the amino terminal end of the peptide, where "acidic" and "basic" are as defined herein. Such modifications are

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well known to increase the α -helical content of the peptide by the "helix dipole effect". They also can provide enhanced aqueous solubility of the peptide. See, e.g., Baldwin et al., supra

As another non-limiting example of a GPR polypeptide of the present invention, serotonergic receptors (5-HT) consensus sequences may be determined using presently known 5-HT sequences and include, e.g., as consensus peptides of TM3, TM5 and TM7, respectively:

5-HT consensus (1) DDDDNISIFDWIGYLNISMVIYTLFKKKK (SEQ ID NO:80)

5-HT consensus (2) DDDDNINIFSTIGYLNISPVSVMHIYGGKKK (SEQ ID NO:81)

10 5-HT consensus (3) DDDDGYSIYDTLVTFAINPVIYITVFKKKK (SEQ ID NO:82)

Such non-naturally occurring consensus sequences may also be further modified according to known method steps to provide additional consensus peptides with substituted amino acids to increase or decrease α -helical propensity and/or solubility (e.g., hydrophilicity). As a non-limiting example, 5-HT consensus peptide (1) above may be modified according to the present invention to have increase helical propensity and increased aqueous solubility as follows:

5-HT consensus (4) DDDDNAWSAFDWALYLNISMALYTYAKKKK (SEQ ID NO:83),

20 wherein, e.g., smaller, non-polar residues replace either larger, more polar residues (e.g., Ala for Ile or Val) or larger aromatic residues (e.g., Ala for Phe).

Another non-limiting, illustrative example of consensus GPR polypeptides of the present invention are those for adrenergic receptors, are the following:

25 An example of the consensus GPR polypeptide for domain VII across all presently known adrenergic receptors is as follows:

adrenergic consensus(1) LFSFITWLGYNSSLNPIIYTTF (SEQ ID NO:84)

30 An example of a consensus GPR polypeptide for domain V across all adrenergic receptors is as follows:

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adrenergic consensus (2) VYTIYSSSVVFFAPSLAIMVITYT (SEQ ID NO:85)

Examples of a consensus GPR polypeptide for domain III across all adrenergic receptors are as follows:

adrenergic consensus (3) IWLTSIDIMSTSSILHNLGVISF (SEQ ID NO:86)

5 An example of a consensus GPR polypeptide for domains III, V, and VII of all adrenergic receptors is as follows:

adrenergic consensus (4) IWSIFSSDIVVGYANHSSLAIMCPIVIYTV (SEQ ID NO:87)

adrenergic consensus (5) IFTIFSSDIAVGYANHSSAAMPFIVIYSV (SEQ ID NO:88),

Wherein variations and substitutions of amino acids may be made as
10 described herein.

Non-limiting examples of consensus GPR polypeptides for transmembrane domain III across several or many, such as 1-500, or any range or value therein, G-protein receptors are as follows:

- TM3- (1) YAIFVLYASAWLSFLNCPFIVTLNI (SEQ ID NO:96)
- 15 TM3- (2) YAIFVLYATAWLSFLNCPFIVTLNI (SEQ ID NO:97)
- TM3- (3) YAIFVLYATAWLTFNCPFIVTLNI (SEQ ID NO:98)
- TM3- (4) YAIFVLYASAWLTFNCPFIVTLNI (SEQ ID NO:99)
- TM3- (5) WAIFVLYASAWLSFLNCPFIVTLNI (SEQ ID NO:100)
- TM3- (6) WAIFVLYATAWLSFLNCPFIVTLNI (SEQ ID NO:101)
- 20 TM3- (7) WAIFVLYATAWLTFNCPFIVTLNI (SEQ ID NO:102)
- TM3- (8) WAIFVLYASAWLTFNCPFIVTLNI (SEQ ID NO:103)
- TM3- (9) YAVFVLYASAWLSFLNMPFIVTLNI (SEQ ID NO:104)
- TM3- (10) YAVFVLYATAWLSFLNMPFIVTLNI (SEQ ID NO:105)
- TM3- (11) YAVFVLYATAWLTFNMPFIVTLNI (SEQ ID NO:106)
- 25 TM3- (12) YAVFVLYASAWLTFNMPFIVTLNI (SEQ ID NO:107)
- TM3- (13) YAIFVLYASAWLSFLNCTASIPFIVTLNI (SEQ ID NO:108)
- TM3- (14) YAIFVLYASAWLSFLNCTSSIVVTASIVTLNI (SEQ ID NO:109)
- TM3- (15) YAIFVLYASAWLSFLNVTNICTSSIV (SEQ ID NO:110)
- TM3- (16) YAIFVLYASAWLSFLNTASILNLMFIVTLNI (SEQ ID NO:111)
- 30 TM3- (17) YAIFVLYASAWLSFLNMASILNLPFIVTLNI (SEQ ID NO:112)
- TM3- (18) YAIFVLYASAWLSFLNSGILLAPFIVTLNI (SEQ ID NO:113)
- TM3- (19) YAIFVLYASAWLSFLNMSGILLAPFIVTLNI (SEQ ID NO:114)
- TM3- (20) YAIFVLYASAWLSFLNSELSVYTTLVCPFIVTLNI (SEQ ID NO:115)
- TM3- (21) YAIFVLYASAWLSFLNMSELSVYTTLVPPFIVTLNI (SEQ ID NO:116)

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) YAIFVLYASAWLASELSVYTLTVSFLNCPFIVTLNI (SEQ ID NO:117)
) YAIFVLYASAWLASELSVYTLTVPPFIVTLNI (SEQ ID NO:118)
) YAIFVLYASAWLSFLASELSVYASELSSTLTTVNMPFIVTLNI (SEQ ID NO:119)
) YAIFVLYASAWLSFLNGGEIALWLSLCPFIVTLNI (SEQ ID NO:120)
) YAIFVLYASAWLSFLNGGEIALWLSLIVTLNI (SEQ ID NO:121)
) YAIFVLYASAWLGGEIALWLSLNCPPFIVTLNI (SEQ ID NO:122)
) YAIFVLYAGGEIALWLSLNCPPFIVTLNI (SEQ ID NO:123)
) YAIFVLYASAWLSFFFLLFGYLGNFLLNCPFIVTLNI (SEQ ID NO:124)
) YAIFVLYASAWLFFFLLFGYLGNFLLPPFIVTLNI (SEQ ID NO:125)
) YAIFVLYASAWLSFLNTACFYVAITASLCFITEIALIPFIVTLNI (SEQ ID NO:126)
) YAIFVLYASAWLTACFYVAITASLCFITEIALICPFIVTLNI (SEQ ID NO:127)
) YAIFVLYATACFYVAITASLCFITEIALISFLNCPFIVTLNI (SEQ ID NO:128)
) YAITACFYVAITASLCFITEIALIASAWLSFLNCPFIVTLNI (SEQ ID NO:129)
) YAIFVLYATACFYVAITEIALISAWLSFLNCPFIVTLNI (SEQ ID NO:130)
) YAIFVLYASAWLSFLNACFYICLFAGVCFLIPFIVTLNI (SEQ ID NO:131)
) YAIFVLYASAWNACFYICLFAGVMFLILSFLNCPFIVTLNI (SEQ ID NO:132)
) YAIFVLYFYICLFAGVCFLIASAWLSFLNCPFIVTLNI (SEQ ID NO:133)
) YAIFVLYASVDVNMFTSAWLSFLNCPFIVTLNI (SEQ ID NO:134)
) YAIFSVDAVNMFVTVLYASAWLSFLNCPFIVTLNI (SEQ ID NO:135)
) YAIFVLYASAWLSVDVNMFTSFLNCPFIVTLNI (SEQ ID NO:136)
) YAIFVLYASAWLSFLNSVDVNMFTPPFIVTLNI (SEQ ID NO:137)
) YAIFVLYASAWLSFLNCPFIVSVDAVNMFITLNI (SEQ ID NO:138)
) YAIFVLYASAWLSVDMFTSFLNCPFIVTLNI (SEQ ID NO:139)
) YAISVDVNMFTFVLYASAWLSFLNCPFIVTLNI (SEQ ID NO:140)
) YAIFSLSVFSLLAIVLYASAWLSFLNCPFIVTLNI (SEQ ID NO:141)
) YAIFVLYASLSVFSLLAISAWLSFLNCPFIVTLNI (SEQ ID NO:142)
) YAIFVLYASAWLSLSVFSLLAISFLNCPFIVTLNI (SEQ ID NO:143)
) YAIFVLYASAWLSFLSLSVFSLLAINCPFIVTLNI (SEQ ID NO:144)
) YAIFVLYASAWLSFLNPFSLSVFSLLAIIVTLNI (SEQ ID NO:145)
) YAIFVLYATAWLTFLNCTVATIPFIVTLNI (SEQ ID NO:146)
) YAIFVLYATAWLSFLNCTSSIVVTATIVTLNI (SEQ ID NO:147)
) YAIFVLYATAWLSFLNVTLNICTTTIV (SEQ ID NO:148)
) YAIFVLYATAWLTFLNTATILNLMFIVTLNI (SEQ ID NO:149)
) YAIFVLYATAWLSFLNMATILNLPFIVTLNI (SEQ ID NO:150)
) YAIFVLYATAWLTFLNSGILLAPFIVTLNI (SEQ ID NO:151)
) YAIFVLYASAWLTFLNMTGILLAPFIVTLNI (SEQ ID NO:152)
) YAIFVLYASAWLTFLNTELTVYTLTVCPFIVTLNI (SEQ ID NO:153)
) YAIFVLYASAWLTFLNMTELTVYTLTVPPFIVTLNI (SEQ ID NO:154)
) YAIFVLYATAWLTATELTVYTLTVTFNCPFIVTLNI (SEQ ID NO:155)
) YAIFVLYASAWLATELSVYTLTVPPFIVTLNI (SEQ ID NO:156)
) YAIFVLYATAWLSFLATELSVYASELSTLTTVNMPFIVTLNI (SEQ ID NO:157)
) YAIFVLYATAWLSFLNGGEIALWTLCPFIVTLNI (SEQ ID NO:158)
) YAIFVLYASAWLTFLNGGEIALWTLIVTLNI (SEQ ID NO:159)
) YAIFVLYASAWLGGEIALWTLNCPFIVTLNI (SEQ ID NO:160)
) YAIFVLYAGGEIALWTLSFLNCPFIVTLNI (SEQ ID NO:161)

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- TM3 - (67) YAIFVLYATAWLSFFFLLFGYLGNFLLNCPFIVTLNI (SEQ ID NO:162)
TM3 - (68) YAIFVLYATAWLFFFLLFGYLGNFLLPFIVTLNI (SEQ ID NO:163)
TM3 - (69) YAIFVLYATAWLTFNLNTACFYVAITASLCFITEIALIPFIVTLNI (SEQ ID NO:164)
TM3 - (70) YAIFVLYATAWLTAFCFYVAITATLCFITEIALICPFIVTLNI (SEQ ID NO:165)
5 TM3 - (71) YAIFVLYATAFCFYVAITATLCFITEIALISFLNCPFIVTLNI (SEQ ID NO:166)
TM3 - (72) YAITACFYVAITASLCFITEIALIATAWLTFNLNCPFIVTLNI (SEQ ID NO:167)
TM3 - (73) YAIFVLYATAFCFYVAIITEIALITAWLTFNLNCPFIVTLNI (SEQ ID NO:168)
TM3 - (74) YAIFVLYASAWLTFNLNACFYICLFAGVCFLIPFIVTLNI (SEQ ID NO:169)
TM3 - (75) YAIFVLYASAWNACFYICLFAGVMFLILTFLNCPFIVTLNI (SEQ ID NO:170)
10 TM3 - (76) YAIFVLYFYICLFAGVCFLIATAWLTFNLNCPFIVTLNI (SEQ ID NO:171)
TM3 - (77) YAIFVLYATVDVNMFTTAWLTFNLNCPFIVTLNI (SEQ ID NO:172)
TM3 - (78) YAIFTVDVNMFTVLYATAWLTFNLNCPFIVTLNI (SEQ ID NO:173)
TM3 - (79) YAIFVLYATAWLTVDAVNMTSFLNCPFIVTLNI (SEQ ID NO:174)
TM3 - (80) YAIFVLYATAWLSFLNTVDVNMFTTPFIVTLNI (SEQ ID NO:175)
15 TM3 - (81) YAIFVLYASAWLTFNLNCPFIVSVDAVNMTTLNI (SEQ ID NO:176)
TM3 - (82) YAIFVLYATAWLSVDMFTTFLNCPFIVTLNI (SEQ ID NO:177)
TM3 - (83) YAVISDAVNMTFFVLYATAWLSFLNCPFIVTLNI (SEQ ID NO:178)
TM3 - (84) YAIFVLYASLTVFSLLAISAWLTFNLNCPFIVTLNI (SEQ ID NO:179)
TM3 - (85) YAIFVLYASAWLTVSVFTLLAISFLNCPFIVTLNI (SEQ ID NO:180)
20 TM3 - (86) YAIFVLYASAWLTVFSLSVFTLLAINCPFIVTLNI (SEQ ID NO:181)
TM3 - (87) YAIFVLYASAWLTVFSLSVFSLLAIVTLNI (SEQ ID NO:182)
TM3 - (88) YAIFVLYASAWLSFLNLGGVTASFTASVGPFIIVTLNI (SEQ ID NO:183)
TM3 - (89) YAIFVLYASAWLSFLNLGGVTASFTASVGVTLNI (SEQ ID NO:184)
TM3 - (90) YAIFVLLGGVTASFTASVNYASAWLSFLNCPFIVTLNI (SEQ ID NO:185)
25 TM3 - (91) YAIFVLYAIFFFLLFSAWLSFLNCPFIVTLNI (SEQ ID NO:186)
TM3 - (92) YAIFVLYASAWLSFLNCPFIVTLNIIFFFLFIVTLNI (SEQ ID NO:187)
TM3 - (93) YAIFVLYASAWIIFFFLLFSLNCPFIVTLNI (SEQ ID NO:188)
TM3 - (94) YAIFVLYASAWLFFTVLASELSVYTLTVSFLNCPFIVTLNI (SEQ ID NO:189)
TM3 - (95) YAIFVLYASAWLSFLFATLGGEIALCPFIVTLNI (SEQ ID NO:190)
30 TM3 - (96) YAIFVLYAFATLGGEIALSAWLSFLNCPFIVTLNI (SEQ ID NO:191)
TM3 - (97) YAIFFTVLASELSVYTLTVYASAWLSFLNCPFIVTLNI (SEQ ID NO:192)
TM3 - (98) YAIFFPIAALFASIASAWLSFLNCPFIVTLNI (SEQ ID NO:193)
TM3 - (99) YAIFVLYASAWLSFFPIAALFASIPFIVTLNI (SEQ ID NO:194)
TM3 - (100) YAIFVLYASAWLSFLNCPFFPIAALFASILNI (SEQ ID NO:195)
35 TM3 - (101) YAIFVLYASAWLSLDVLFSTASIMHLSFLNGGEIALWSLIVTLNI (SEQ ID NO:196)
TM3 - (102) YAIFVLYASLDVLFSTASIMHLIALWSLNCPPFIVTLNI (SEQ ID NO:197)
TM3 - (103) YAIFVLYAGGEIALWSLSFLNSLDVLFSTASIMHLPFIVTLNI (SEQ ID NO:198)
TM3 - (104) YAIFVLYASAWLSFFDVLFSTASIMHLFGYLGNFLLNCPFIVTLNI (SEQ ID NO:199)
TM3 - (105) YAIFVLYASAWLFFFLLFGYLSLDVLFSTASIMHLGNFLLPFIVTLNI (SEQ ID NO:200)
40 TM3 - (106) YAIFVLYASAWLSFLNTACFYVAITASLSIMHLFITEIALIPFIVTLNI (SEQ ID NO:201)
TM3 - (107) YASLDVLFSTAIMHLSAWLTACFYVAITASLCFITEIALICPFIVTLNI (SEQ ID NO:202)
TM3 - (108) YAIFVLYATAFCFYVAITASLSFLNCPFIVTLNISLDVLFSTASIMHL (SEQ ID NO:203)
TM3 - (109) YAITACFYVAITASLCFITEIALIASAWLSFLNCPFIVTLNI (SEQ ID NO:204)
TM3 - (110) YAIFVLYATAFCFYSTASILNIMHLCAISLVAIITEIALISAWLSFLN (SEQ ID NO:205)
45 TM3 - (111) YAIFVLYASAWLSFLNACFYICLFASILNIMHLGVCFLIPFIVTLNI (SEQ ID NO:206)

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- TM3 - (112) YAIFVLYASAWNASILNLMHLFCFYICLFAGVMLILSFLNCPFIVTLNI (SEQ ID NO:207)
 TM3 - (113) YAIFPFVQCVCVSIFSLVLIADVLYFYIAGVCFLIASAWLSFLNCPFIVTI (SEQ ID NO:208)
 TM3 - (114) PFVQCVSITVSIFSLVLIADVYAIFVLYASVDAVNMFSAWCPFIVTLNI (SEQ ID NO:209)
 TM3 - (115) YAIFGDWSSVDAVNMFVLYASAWLSFLNCPFIVTLNI (SEQ ID NO:210)
 5 TM3 - (116) YAIFVLYAGDWSSAWLSVDAVNMFSTFLNCPFIVTLNI (SEQ ID NO:211)
 TM3 - (117) YAIFVLYASAWLGDWSSFLNSVDAVNMFPPFIVTLNI (SEQ ID NO:212)
 TM3 - (118) YAIFVLYASAWLSFLNCPFIVGDWSSVDAVNMFVTLNI (SEQ ID NO:213)
 TM3 - (119) YAIFVLYASAWLGYLGSDVMFTSFLNCPFIVTGDWSLNI (SEQ ID NO:214)
 TM3 - (120) YAI SVDVNMFVLYAGYLGSAWLSFLNCPFIVTLNI (SEQ ID NO:215)
 10 TM3 - (121) YAI FLSVFSLLAIVLYASAWLGYLGSAWLSFLNCPFIVTLNI (SEQ ID NO:216)
 TM3 - (122) YAIFVLYAGYLGAGNMDLSVFSLLAISAWLSFLNCPFIVTLNI (SEQ ID NO:217)
 TM3 - (123) YAIFVLYASAWLSLSVFGNMSLLAISFLNCPFIVTLNI (SEQ ID NO:218)
 TM3 - (124) YAIFVLYASAWLSFLSLSVFGSLLAINCPFIVTLNI (SEQ ID NO:219)
 TM3 - (125) YAIFVLYASAWLSFLNPFSLSVFGSLLAIVTLNI (SEQ ID NO:220)
 15 TM3 - (126) YAIFVLYATAWLTFLSLANCVTATIPFIVTLNI (SEQ ID NO:221)
 TM3 - (127) YAIFVLYATAWLSFLNCTSLASSIVVTATIVTLNI (SEQ ID NO:222;
 TM3 - (128) YAIFVLYATAWLSFLNVTLNISLACTTTIV (SEQ ID NO:223)
 TM3 - (129) YAIFVLYATAWLTFLNTATILSLANLMFIVTLNI (SEQ ID NO:224)
 TM3 - (130) YAIFVLYATAWLSFLNMTILNLPFSVDAVIVTLNI (SEQ ID NO:225)

- 20 Recently discovered G-proteins also can be used according to the presently claimed invention to provide GPR polypeptides of the present invention, based on the teaching and guidance presented herein. Exemplified of such GPR polypeptides of the present invention may include, as non-limiting examples, GPR polypeptides corresponding to transmembrane domain III, e.g., as follows:
- 25

- TM3 - (131) ISTMYTVTGRWTLGQVVCDFWLSSDITCCTASILHLCVIAL (SEQ ID NO:226)
 TM3 - (132) ILYGYRWPLPSKLCVAVWIYLDVLFSTASIMHLCAISL (SEQ ID NO:227)
 TM3 - (133) IYYI VMDRWKLGFLCEVWLSVDMTCCTCSILHLCVIAL (SEQ ID NO:228)
 TM3 - (134) IADKTVRVAMGAENDLGYNFRSDDVCCHCWQWYCSL (SEQ ID NO:229)
 30 TM3 - (135) ILNYWPFGLALCHFVNYSQAVSVLVSAYTLVAISI (SEQ ID NO:230)
 TM3 - (136) ILGRWEFGIHLCKLWLTCDVLCCTSSILNLCAIALD (SEQ ID NO:231)
 TM3 - (137) IMASVMHRHCLPLIGICLSSERHCLVSIFVELGAL (SEQ ID NO:232)

- Further non-limiting examples of consensus GPR polypeptides for transmembrane domain III of several or many, such as 1-500, or any range or value therein, more recently discovered G-protein receptors are as follows:
- 35

- TM3 - (138) YAIFVLYASAWLSFLNCPFISILHLCVIALVTLNI (SEQ ID NO:233)
 TM3 - (139) YAIFVLYATAWLSFLNCPFISILNLCAIALDVTLNI (SEQ ID NO:234)

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- TM3- (140) YAIFVLYATAWLTFNLCPFISIFVELGALVTLNI (SEQ ID NO:235)
 TM3- (141) YAIFVLYASAWLTFNLCPFISIFVELSIMHLCAISLGALVTLNI (SEQ ID NO:236)
 TM3- (142) WAIFVLYAILGRWEFGIHLCKLWLTSAWLSIMHLCAISLSFLNCPFIVTLNI (SEQ ID NO:237)
 TM3- (143) WAIFVLYAILGRWEFGIHLCKLWLTTAWLSIMHLCAISLSFLNCPFIVTLNI (SEQ ID NO:238)
 5 TM3- (144) WAIFVLYATAWLTFNLCPFSIMHLCAISLIVTLNI (SEQ ID NO:239)
 TM3- (145) WAIFVLYASAWLTFNLCPFISIMHLCAISLVTNI (SEQ ID NO:240)
 TM3- (146) YAVFVLYASAWLSFLNMSIMHLCAISLPFIVTLNI (SEQ ID NO:241)
 TM3- (147) YAVFVLYATAWLSFLNMPFSILNLCAIALDIVTLNI (SEQ ID NO:242)
 TM3- (148) YAVFVLYATAWLSILNLCAIALDTFLNMPFIVTLNI (SEQ ID NO:243)
 10 TM3- (149) YAVFVLYASILNLCAIALDSAWLTFLNMPFIVTLNI (SEQ ID NO:244)
 TM3- (150) YAIFVLYASAWLSFLNCVTASIPFCLVSIFVELGALIVTLNI (SEQ ID NO:245)
 TM3- (151) YAIFVLYASAWLSFLNCLVSIFVELGALIVVTASIVTLNI (SEQ ID NO:246)
 TM3- (152) YAIFVLYASAWLSFLNVTNLCLVSIFVELGALII (SEQ ID NO:247)
 TM3- (153) YAIFVLYASAWLSFLNTASILNLMFICLVSIIFVELGALVTLNI (SEQ ID NO:248)
 15 TM3- (154) YAIFVLYASAWLSFLNMAISILNLPFCLVSIFVELGALVTLNI (SEQ ID NO:249)
 TM3- (155) YAIFVLYASAWLSFLNILGRWEFGIHLCKLWLTCDVLCCTSSGILLAPFIVTLNI (SEQ ID NO:250)
 TM3- (156) YAIFVLYASAWLSFLNMIILGRWEFGIHLCKLWLTCDVLCCTSSGILLAPFIVTLNI (SEQ ID NO:251)
 TM3- (157) YAIFVLYASAWLILGRWEFGIHLCKLWLTCDVLCCTSSFLNSELSVYTLTVCPFIVTLNI (SEQ ID NO:252)
 20 TM3- (158) YAIFVLYAILGRWEFGIHLCKLWLTCDVLCCTSSAWLSFLNMSSELSVYTLTVPPFIVTLNI (SEQ ID NO:253)
 TM3- (159) YAIFVLYASAWLASRWPLPLSVYTLTVSFLNCPFIVTLNI (SEQ ID NO:254)
 TM3- (160) YAIFVLYASAWLASELILYYWRWPLPCLHDLVWLCTCSILHLCVIALSVYTLTVPPFIVTLNI (SEQ ID NO:255)
 25 TM3- (161) YAIFVLYASAWLSFLASELSVYASELSSTLHDLVWLWLDVFCVIALTTVNMPFIVTLNI (SEQ ID NO:256)
 TM3- (162) YAIFVLYASAWLSFLNGGEIALWSLCPFIILYYWRWPLPCLHDLVLSILHLCVIALVTLNI (SEQ ID NO:257)
 TM3- (163) YVWLWLDVFCCTCSILHLCVIALFVLYASAWLSFLNGGEIALWSLIVTLNI (SEQ ID NO:258)
 30 TM3- (164) YAIFVLYASAWLAIIILYYWRWPLPCLHDLGGEIALWSLNCPPFIVTLNI (SEQ ID NO:259)

Non-limiting examples of consensus GPR polypeptides for domain V across several or many, such as 1-500, or any range or value therein, G-protein receptors are as follows:

- TM5- (1) CDVVFVVDIMLCTASIFNLCAISVG (SEQ ID NO:260)
 35 TM5- (2) YAIFVLYDIMLCTASIFNLCAISVG (SEQ ID NO:261)
 TM5- (3) DYAIFFVVDIMLMTASIFNLMAISVG (SEQ ID NO:262)
 TM5- (4) DYAIFFVVDIMLHTTASTIFNLMTITVG (SEQ ID NO:263)
 TM5- (5) CDVAVVYSSDIMLFYVCTASIFSSNLCAISSVG (SEQ ID NO:264)
 TM5- (6) FLFCSLGSFYIPIAVILVDIMLCTASIFNLCAISVG (SEQ ID NO:265)
 40 TM5- (7) YAIFVLYDFLFCSLGSFYIPIAVILIMLCTASIFNLCAISVG (SEQ ID NO:266)
 TM5- (8) DYAIFFVVDIMLMTASIFLFCSLGSFYIPIAVILISVG (SEQ ID NO:267)
 TM5- (9) DYAIFFVVDIMLHTTASTIFNLMAFLFCSLGSFYIPIAVILTITVG (SEQ ID NO:268)

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- TM5 - (10) CDVAVVYSSDIMLFYVCTASIFSSNLFCSLGSFYCAISSVG (SEQ ID NO:269)
TM5 - (11) CDVVFVVDIMLCTASIFNWIYILSSIGSFAPCLILLVYLLCAISVG (SEQ ID NO:270)
TM5 - (12) YAIFVLYDIMLCTASIFNLCAIWIYILSSIGSFAPCLILLVYLSVG (SEQ ID NO:271)
TM5 - (13) DYAIFFVVDIWIYILSSIGSFAPCLILLVYLASIFNLMAISVG (SEQ ID NO:272)
5 TM5 - (14) DYAIWIYILSSIGSFAPCLILLVYLIMLHTTASTIFNLMATITVG (SEQ ID NO:273)
TM5 - (15) CDVAVVYSSDIMLFYVCWIYILSSIGSFAPCLILLVYLSSNLCAISSVG (SEQ ID NO:274)
TM5 - (16) CDVVFVVDIMLCTASIFWYVISSSIGSFAPCLINHLVYNLCAISVG (SEQ ID NO:275)
TM5 - (17) YAIFVLYDIMLCTASIFNLCAIWIYVISSSIGSFAPCLINHLVYSVG (SEQ ID NO:276)
TM5 - (18) DYAIFFVFWYVISSSIGSFAPCLINHLVYDIMLMTASIFNLMAISVG (SEQ ID NO:277)
10 TM5 - (19) DYAIFFVVDIMLHTTASTIFWYVISSSIGSFAPCLINHLVYTVG (SEQ ID NO:278)
TM5 - (20) CDVAVVYSSDIMLFYVCTASIFSWYVISIGSFAINHLVYNLCAISSVG (SEQ ID NO:279)
TM5 - (21) CDVVFVVDIMLCTASIFNLCAITYAISSSVISFYIPVAILVTTYT (SEQ ID NO:280)
TM5 - (22) YAIFVLYDIMLCTATYAISSSVISFYIPVAILVTTYTSIFNLCAISVG (SEQ ID NO:281)
TM5 - (23) DYAIFFVVDIMLMTATYAISSSVISFYIPVAILVTTYTISVG (SEQ ID NO:282)
15 TM5 - (24) TYAISSSVISFYIPVATDYAIFFVVDIMLHTTASTIFNLMATITVG (SEQ ID NO:283)
TM5 - (25) CDVAVVYSSDIMLFYVCTATYAISSSVISFYIPVAILVTTYTSSVG (SEQ ID NO:284)
TM5 - (26) CDVVFVVDIFYSSVVSFYLPFGVTVLVYACTASIFNLCAISVG (SEQ ID NO:285)
TM5 - (27) YAIFVLYDFVIYSSVVSFYLPFGVTVLVYASIFNLCAISVG (SEQ ID NO:286)
TM5 - (28) DYAIFFVVDIFYSSVVSFYLPFGVTVLVYATASIFNLMAISVG (SEQ ID NO:287)
20 TM5 - (29) DYAIFFVVDIFYSSVVSFYLPFGVTVLVYHTTASTIFNLMATITVG (SEQ ID NO:288)
TM5 - (30) CDVAVVYSSDIFYSSVVSFYLPFGVTVVYCTASIFSSNLCAISSVG (SEQ ID NO:289)
TM5 - (31) CDVVFVVDIMLCTASYTTIYSTCGAFYIPSVLLIILYGNLCAISVG (SEQ ID NO:290)
TM5 - (32) YAIFVLYDIMLCTASYTTIYSTCGAFYIPSVLLIILYGNLCAISVG (SEQ ID NO:291)
TM5 - (33) DYAIFFVVDIMLMTASYTTIYSTCGAFYIPSVLLIILYGNLMAISVG (SEQ ID NO:292)
25 TM5 - (34) DYAIFFVVDIMLHTTASYTTIYSTCGAFYIPSVLLIILYGMATITVG (SEQ ID NO:293)
TM5 - (35) CDVAVVYSSDIMSYTTIYSTCGAFYIPSVLLIILYGFSSNLCAISSVG (SEQ ID NO:294)
TM5 - (36) CDVVFVFLIGSFVAVDIMLCTASIFNLCAISVG (SEQ ID NO:295)
TM5 - (37) YAIFVLYFVLIGSFVADIMLCTASIFNLCAISVG (SEQ ID NO:296)
TM5 - (38) DYAIFFVFLIGSFVADIMLMTASIFNLMAISVG (SEQ ID NO:297)
30 TM5 - (39) DYAIFFVFLIGSFVADIMLHTTASTIFNLMATITVG (SEQ ID NO:298)
TM5 - (40) CDVAVVYSSFVLIGSFVADIMLFYVCTASIFSSNLCAISSVG (SEQ ID NO:299)
TM5 - (41) CDVVFVVDIMLCFFIPTLIMVITYFNLCAISVG (SEQ ID NO:300)
TM5 - (42) YAIFVLYDIMLCFFIPTLIMVITYFNLCAISVG (SEQ ID NO:301)
TM5 - (43) DYAIFFVVDIMLMFFIPTLIMVITYFNLMAISVG (SEQ ID NO:302)
35 TM5 - (44) DYAIFFVVDIMLHTFFIPTLIMVITYFNLMATITVG (SEQ ID NO:303)
TM5 - (45) CDVAVVYSSDIMLFYVCFIPTLIMVITYFSSNLCAISSVG (SEQ ID NO:304)
TM5 - (46) CDVVYGLVDGLVTFYLPLLIMCITYYDIMLCTASIFNLCAISVG (SEQ ID NO:305)
TM5 - (47) YAIYVGLVDGLVTFYLPLLIMCITYYDIMLCTASIFNLCAISVG (SEQ ID NO:306)
TM5 - (48) DYAIYVGLVDGLVTFYLPLLIMCITYYDIMLMTASIFNLMAISVG (SEQ ID NO:307)
40 TM5 - (49) DYAIYVGLVDGLVTFYLPLLIMCISSDIMLHTTASTIFNLMATITVG (SEQ ID NO:308)
TM5 - (50) CDVVYDGLVTFYLPLLIMCITYYDIMLFYVCTASIFSSNLCAISSVG (SEQ ID NO:309)
TM5 - (51) CDVVFVVDIMLLVIFLGLVIVIPFVLIIVSYAIFNLCAISVG (SEQ ID NO:310)
TM5 - (52) YAIFVLYDIMLLVIFLGLVIVIPFVLIIVSYAIFNLCAISVG (SEQ ID NO:311)
TM5 - (53) DYAIFFVVDIMLLVIFLGLVIVIPFVLIIVSYAIFNLMAISVG (SEQ ID NO:312)
45 TM5 - (54) DYAIFFVVDIMLHTLVIFLGLVIVIPFVLIIVSYAIFNLMATITVG (SEQ ID NO:313)

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- TM5- (55) CDVAVVYSSDIMLFLVIFLGLVIVIPFVLIIVSYAIFSSNLCAISSVG (SEQ ID NO:314)
 TM5- (56) CDVVFVVDIMLCTALMIYILGGLIIIIIPFLLIVMSYVSIFNLCAISVG (SEQ ID NO:315)
 TM5- (57) YAIFVLYDIMLCTALMIYILGGLIIIIIPFLLIVMSYVSIFNLCAISVG (SEQ ID NO:316)
 TM5- (58) DYAIFVVDIMLMTASIFNLMYILGGLIIIIIPFLLIVMSYVLMASVG (SEQ ID NO:317)
 5 TM5- (59) DYAIFVVDIMLHTTASTILMIYILGGLIIIIIPFLLIVMSYVITVG (SEQ ID NO:318)
 TM5- (60) CDVAVVYSSDIMLFFVCTAYILGGLIPFLLIVMTYVSIFTNLCAISSVG (SEQ ID NO:319)
 TM5- (61) CDVVFVVDIMLCTASIFNLLMIHIMEVIIIVIPFVLIVISYACASVG (SEQ ID NO:320)
 TM5- (62) YAIFVLYDIMLCTASIFNLLMIHIMEVIIIVIPFVLIVISYACASVG (SEQ ID NO:321)
 TM5- (63) DYAIFVVDIMLMTASIFLMIHIMEVIIIVIPFVLIVISYASVG (SEQ ID NO:322)
 10 TM5- (64) DYAIFVVDIMLHTTASTILMIHIMEVIIIVIPFVLIVISYAITVG (SEQ ID NO:323)
 TM5- (65) CDVAVVYSSDIMLFFVCTASIFLMIHIMEVIIIVIPFVLIVISYAAISSVG (SEQ ID NO:324)

Non-limiting examples of longer consensus GPR polypeptides for domain V across several or many, such as 1-500, or any value or range therein, G-protein receptors are as follows:

- 15 T M 1 - (1)
 TM1NWPALSIVVIIINTIGGNILVIMAVSIYTSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLNFFVFW
 IGYVCSSSLGINPVIIYTLF (SEQ ID NO:325)
 T M 1 - (2)
 NWPALSIVVIIINTIGGNILVIMAVTIYTTLDVMLCTATILNLLISLFLVIGTFVAFFIPLTIMVITYFLNFFVFWIGY
 20 VCTTTLGINPVIIYTLF (SEQ ID NO:326)
 T M 1 - (3)
 NWPALTIVVIIINTIGGNILVIMAVSIYTTLDVMLCTATILNLLITLFLVIGTFVAFFIPLTIMVITYFLNFFVFWIGY
 VCSTSLGINPVIIYTLF (SEQ ID NO:327)
 T M 1 - (5)
 25 NWPALTIVVIIINTIGGNILVIMAVTIYTTLDVMLCTATILNLLITLFLVIGTFVAFFIPLTIMVITYFLNFFVFWIGY
 VCTLGINPVIIYTLF (SEQ ID NO:328)
 T M 1 - (6)
 NWKNWSALLITTVVIIITAGNIIIVIMAVSSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLNFFVFWIGY
 VCSSSLGINPVIIYTLF (SEQ ID NO:329)
 30 T M 1 - (7)
 ITITVVLAVLILITVAGNVVVCIAVGSYTSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLNFFVFWIG
 YVCSSSLGINPVIIYTLF (SEQ ID NO:330)
 T M 1 - (8)
 TLTLCIACLSLTVFGNVLVIIAVFSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLNFFVFWIGYVCS
 35 SSLGINPVIIYTLF (SEQ ID NO:331)
 T M 1 - (9)
 TAAIAAAITFLILFTIFGNALVIIAVLSIYTSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLNFFVFWI
 GYVCSSSLGINPVIIYTLF (SEQ ID NO:332)
 T M 1 - (1 0)
 40 AISVGLVLGAFILFAIVGNILVILSVANWPALSIVVIIINTIGGNILVIMAVSIYTSLDVMLCTASILNLLISLFLVIGS
 FVAFFIPLTIMVITYFLNFFVFWIGYVCSSSLGINPVIIYTLF (SEQ ID NO:333)

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T M 1 - (1 1)
 AALAGALLALAVLATVGGNLLVIVAIASLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLFNFFVWIGYVC
 SSSLGINPVIIYTLF (SEQ ID NO:334)

5 T M 1 - (1 2)
 TAGDCLIMLIVLLIVAGNVLVIVAIASLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLFNFFVWIGYVCSS
 SLGINPVIIYTLF (SEQ ID NO:335)

T M 1 - (1 3)
 VITIAVVTAVVSLMTIVGNVLVMSFSIYTSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLFNFFVWIG
 YVCSSSLGINPVIIYTLF (SEQ ID NO:336)

10 T M 1 - (1 4)
 MVFIATVRGSLSLVTVVGNIIVMLISISYTSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLFNFFVWIG
 YVCSSSLGINPVIIYTLF (SEQ ID NO:337)

T M 1 - (1 5)
 WFIAFLTIGILALVTIIGNILVIVSFSIYTSLDVMLCTASILNLLISLFLVIGSFVAFFIPLTIMVITYFLFNFFVWIGY
 15 VCSSSLGINPVIIYTLF (SEQ ID NO:338)

Non-limiting examples of longer consensus GPR polypeptides
 for domain V across several or many, such as 1-500, or any value or
 range therein, G-protein receptors are as follows:

T M 3 - (1 6 5)
 20 NWPALSIVVIIINTIGGNILVIMAFFACFVLVLTQSSIFSLAIAINLLISLFLVIGSFVAFFIPLTIMVITYFLFNFF
 VWIGYVCSSSLGINPVIIYTLF (SEQ ID NO:339)

T M 3 - (1 6 6)
 NWPALSIVVIIINTIGGNILVIMAFFACFVLVLTQSSIFSLAIAIAFVLIGSFVAFFIPLTIMVITYFLFNFFVWIGYV
 CSSLGINPVIIYTLF (SEQ ID NO:340)

25 T M 3 - (1 6 7)
 NWPALSIVVIIINTIGGNILVIMAVMVACPVILILTQSSIIALLAIAVSFVAFFIPLTIMVITYFLFNFFVWIGYVCSS
 LGINPVIIYTLF (SEQ ID NO:341)

T M 3 - (1 6 8)
 NWPALSIVVIIINTIGGNILVIMAVLWLALDYVASNASVLNLLISFFFIPLTIMVITYFLFNFFVWIGYVCSSSLGIN
 30 PVIIYTLF (SEQ ID NO:342)

T M 3 - (1 6 9)
 NWPALSIVVIIINTIGGNILVIMAVLYVVSNASVMNLLIISFVAFFIPLTIMVITYFLFNFFVWIGYVCSSSLGINPV
 IYTLF (SEQ ID NO:343)

T M 3 - (1 7 0)
 35 NWPALSIVVIIINTIGGNILVIMAVLWIAIDYVASNASVLNLLVISFGSFVAFFIPLTIMVITYFLFNFFVWIGYVCSS
 SLGINPVIIYTLF (SEQ ID NO:344)

T M 3 - (1 7 1)
 NWPALSIVVIIINTIGGNILVIMAVLFPFLQKSSVGITVLNLCALSGSFVAFFIPLTIMVITYFLFNFFVWIGYVCSS
 LGINPVIIYTLF (SEQ ID NO:345)

40 T M 3 - (1 7 2)
 NWPALSIVVIIINTIGGNILVIMAVCITYLQYLGINASSCSITAFTIIGSFVAFFIPLTIMVITYFLFNFFVWIGYVCS
 SSLGINPVIIYTLF (SEQ ID NO:346)

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T M 3 - (1 7 3)
 NWPALSIVVIIINTIGGNILVIMAVFHNFFPIAALFASIYSMTAVAGSFVAFFIPLTIMVITYFLFNVFFVWIGYVCSSS
 LGINPVIIYTLF (SEQ ID NO:347)
 T M 3 - (1 7 4)
 5 NWPALSIVVIIINTIGGNILVIMAVIASASVSFNLYASVFLLTCLSIGSFVAFFIPLTIMVITYFLFNVFFVWIGYVCSS
 SLGINPVIIYTLF (SEQ ID NO:348)

As another non-limiting, illustrative example of a GPR polypeptide consensus sequences across each individual or different transmembrane domains of 5-HT receptors may be made, such as for 5-HT, as the following:

5HT consensus(4) KNASALLSVIIINSIGGNVVTAVS (SEQ ID NO:349);
 5HT consensus(5) YFLMSLAVTDLVVSFVMPVSAL (SEQ ID NO:350);
 5HT consensus(6) AITKIAITWAISGVSVFPFIPVWG (SEQ ID NO:351); and
 15 5HT consensus(7) LGIIFGTFIIIWLPFFITNLVSP (SEQ ID NO:352);

Wherein variations and substitutions of amino acids may be made as described herein.

Alternatively, 5-HT consensus sequences may be provided as consensus peptides of the present invention as consensus peptides for individual transmembrane domains, such as 5-HT domains III, V and VII, e.g., as follows:

5-HT consensus (8): IWISLDVLFSTASSIMHLCAISL (SEQ ID NO:353)
 5-HT consensus (9): GYTIYSTLVTFYIPSVIMVITYG (SEQ ID NO:354)
 5-HT consensus (10): LLNFFNWIGYLNLSLNPVIYTLF (SEQ ID NO:355)

25 This invention is also directed to an antibody which binds an epitope specific for a GPR polypeptide of the present invention and the use of such an antibody to detect the presence of, or measure the quantity or concentration of, the GPR protein in a cell, a cell or tissue extract, a biological fluid, an extract thereof, a solution, or sample, in vitro, in situ, or in vivo.

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The term "antibody" is meant to include polyclonal antibodies, monoclonal antibodies (mAbs), chimeric antibodies, anti-idiotypic (anti-Id) antibodies to antibodies specific for GPR polypeptide of the present invention, as well as fragments, consensus polypeptides or chemical derivatives thereof.

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen.

A monoclonal antibody contains a substantially homogeneous population of antibodies specific to antigens, which population contains substantially similar epitope binding sites. MABs may be obtained by methods known to those skilled in the art. See, for example Kohler and Milstein, *Nature* 256:495-497 (1975); U.S. Patent No. 4,376,110; Ausubel et al, eds., *Current Protocols in Molecular Biology*, Wiley Interscience, N.Y., (1987, 1992); and Harlow and Lane *Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory (1988), the contents of which references are incorporated entirely herein by reference. Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, GILD and any subclass thereof. A hybridoma producing a mAb of the present invention may be cultivated *in vitro*, *in situ* or *in vivo*. Production of high titers of mAbs *in vivo* or *in situ* makes this the presently preferred method of production.

Chimeric antibodies are molecules different portions of which are derived from different animal species, such as those having variable region derived from a murine mAb and a human immunoglobulin constant region, which are primarily used to reduce immunogenicity in application and to increase yields in production, for example, where murine mAbs have higher yields from hybridomas but higher immunogenicity in humans, such that human/murine chimeric mAbs are used. Chimeric antibodies and methods for their production are known in the art (Cabilly et al, *Proc. Natl. Acad. Sci. USA* 81:3273-3277 (1984); Morrison et al., *Proc. Natl. Acad. Sci. USA* 81:6851-6855 (1984); Boulianne et al., *Nature* 312:643-646 (1984); Cabilly et al., *European Patent Application* 125023 (published November 14, 1984); Neuberger et al., *Nature* 314:268-270 (1985); Taniguchi et al., *European Patent Application* 171496 (published February 19, 1985);

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Morrison et al., *European Patent Application 173494* (published March 5, 1986); Neuberger et al., *PCT Application WO 86/01533*, (published March 13, 1986); Kudo et al., *European Patent Application 184187* (published June 11, 1986); Morrison et al., *European Patent Application 173494* (published March 5, 1986); Sahagan et al., *J. Immunol.* 137:1066-1074 (1986); Robinson et al., *International Patent Publication No. PCT/US86/02269* (published 7 May 1987); Liu et al., *Proc. Natl. Acad. Sci. USA* 84:3439-3443 (1987); Sun et al., *Proc. Natl. Acad. Sci. USA* 84:214-218 (1987); Better et al., *Science* 240:1041-1043 (1988); and Harlow and Lane *Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory (1988)). These references are incorporated entirely herein by reference.

An anti-idiotypic (anti-Id) antibody is an antibody which recognizes unique determinants generally associated with the antigen-binding site of an antibody. An Id antibody can be prepared by immunizing an animal of the same species and genetic type (e.g., mouse strain) as the source of the mAb with the mAb to which an anti-Id is being prepared. The immunized animal will recognize and respond to the idiotypic determinants of the immunizing antibody by producing an antibody to these idiotypic determinants (the anti-Id antibody). See, for example, U.S. patent No. 4,699,880, which is herein entirely incorporated by reference.

The anti-Id antibody may also be used as an "immunogen" to induce an immune response in yet another animal, producing a so-called anti-anti-Id antibody. The anti-anti-Id may be epitopically identical to the original mAb which induced the anti-Id. Thus, by using antibodies to the idiotypic determinants of a mAb, it is possible to identify other clones expressing antibodies of identical specificity.

Accordingly, mAbs generated against a GPR polypeptide of the present invention may be used to induce anti-Id antibodies in suitable animals, such as BALB/c mice. Spleen cells from such immunized mice are used to produce anti-Id hybridomas secreting anti-Id mAbs. Further, the anti-Id mAbs can be coupled to a immunogenic carrier such as keyhole limpet hemocyanin (KLH) or cationized bovine serum albumin and used to immunize additional BALB/c mice. Sera from these mice will contain anti-anti-Id antibodies that have the binding

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properties of the original mAb specific for a GPR polypeptide epitope.

The anti-Id mAbs thus have their own idiotypic epitopes, or "idiotopes" structurally similar to the epitope being evaluated.

5 The term "antibody" is also meant to include both intact molecules as well as fragments thereof, such as, for example, Fab and F(ab')₂, which are capable of binding antigen. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding
10 than an intact antibody (Wahl et al., *J. Nucl. Med.* 24:316-325 (1983)).

It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies useful in the present invention may be used for the detection and quantitation of a GPR polypeptide
15 according to the methods disclosed herein for intact antibody molecules. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments).

An antibody is said to be "capable of binding" a molecule
20 if it is capable of specifically reacting with the molecule to thereby bind the molecule to the antibody. The term "epitope" is meant to refer to that portion of any molecule capable of being bound by an antibody which can also be recognized by that antibody. Epitopes or "antigenic determinants" usually consist of chemically
25 active surface groupings of molecules such as amino acids, lipids or sugar side chains and have specific three dimensional structural characteristics as well as specific charge characteristics.

An "antigen" is a molecule or a portion of a molecule capable of being bound by an antibody which is additionally capable
30 of inducing an animal to produce antibody capable of binding to an epitope of that antigen. An antigen may have one, or more than one epitope. The specific reaction referred to above is meant to indicate that the antigen will react, in a highly selective manner, with its corresponding antibody and not with the multitude of other
35 antibodies which may be evoked by other antigens.

The antibodies, or fragments of antibodies, useful in the present invention may be used to quantitatively or qualitatively

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detect a GPR polypeptide in a sample or to detect presence of cells which express a GPR polypeptide of the present invention. This can be accomplished by immunofluorescence techniques employing a fluorescently labeled antibody (see below) coupled with light
5 microscopic, flow cytometric, or fluorometric detection.

The antibodies (of fragments thereof) useful in the present invention may be employed histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of a GPR polypeptide of the present invention. *In situ* detection may be
10 accomplished by removing a histological specimen from a patient, and providing the a labeled antibody of the present invention to such a specimen. The antibody (or fragment) is preferably provided by applying or by overlaying the labeled antibody (or fragment) to a biological sample. Through the use of such a procedure, it is
15 possible to determine not only the presence of a GPR polypeptide but also its distribution on the examined tissue. Using the present invention, those of ordinary skill will readily perceive that any of wide variety of histological methods (such as staining procedures) can be modified in order to achieve such *in situ* detection.

20 Such assays for a GPR polypeptide of the present invention typically comprise incubating a biological sample, such as a biological fluid, a tissue extract, freshly harvested cells such as lymphocytes or leukocytes, or cells which have been incubated in tissue culture, in the presence of a detectably labeled antibody
25 capable of identifying a GPR polypeptide, and detecting the antibody by any of a number of techniques well-known in the art. See, e.g., Harlow and Lane, supra; Ausubel et al, supra; and Sambrook et al, supra.

The biological sample may be treated with a solid phase
30 support or carrier, such as nitrocellulose, or other solid support or carrier which is capable of immobilizing cells, cell particles or soluble proteins. The support or carrier may then be washed with suitable buffers, followed by treatment with a detectably labeled GPR polypeptide-specific antibody. The solid phase support or carrier
35 may then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on said solid support or carrier

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may then be detected by known method steps, see, e.g., Harlow, supra; Ausubel, supra; or Sambrook, supra.

By "solid phase support", "solid phase carrier", "solid support", "solid carrier", "support" or "carrier" is intended any support or carrier capable of binding antigen or antibodies. Well-known supports or carriers, include glass, polystyrene, polypropylene, polyethylene, dextran, nylon amyloses, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support or carrier configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, polymer test strip, etc. Preferred supports or carriers include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

The binding activity of a given lot of anti-GPR polypeptide antibody may be determined according to well known method steps. Those skilled in the art will be able to determine operative and optimal assay conditions for each determination by employing routine experimentation. See, e.g., Harlow, supra.

Other such steps as washing, stirring, shaking, filtering and the like may be added to the assays as is customary or necessary for the particular situation.

One of the ways in which a GPR polypeptide-specific antibody, anti-idiotypic antibody or fragment thereof, can be detectably labeled is by linking the same to an enzyme and use in an enzyme immunoassay (EIA). This enzyme, in turn, when later exposed to an appropriate substrate, will react with the substrate in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorometric or by visual means. Enzymes which can be used detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease,

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delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-
5 6- phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods which employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared
10 standards. See, Harlow, supra, Ausubel, supra.

Detection may be accomplished using any of a variety of other immunoassays. For example, by radioactivity labeling the antibodies or antibody fragments, it is possible to detect R-PTPase through the use of a radioimmunoassay (RIA). A good description of
15 RIA maybe found in *Laboratory Techniques and Biochemistry in Molecular Biology*, by Work et al., North Holland Publishing Company, NY (1978) with particular reference to the chapter entitled "An Introduction to Radioimmune Assay and Related Techniques" by Chard, incorporated entirely by reference herein. The radioactive isotope
20 can be detected by such means as the use of a γ -counter, a scintillation counter or by autoradiography.

It is also possible to label an anti-GPR polypeptide antibody, anti-idiotypic antibody or fragment thereof, with a fluorescent compound. When the fluorescently labeled antibody is
25 exposed to light of the proper wave length, its presence can be then be detected due to fluorescence. Among the most commonly used fluorescent labelling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine, commercially available, e.g., from
30 Molecular Probes, Inc. (Eugene, Ore.).

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu , or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriamine pentaacetic
35 acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the

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chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, 5 imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. 10 The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

An antibody molecule of the present invention may be adapted for utilization in a immunometric assay, also known as a 15 "two-site" or "sandwich" assay. In a typical immunometric assay, a quantity of unlabeled antibody (or fragment of antibody) is bound to a solid support or carrier and a quantity of detectably labeled soluble antibody is added to permit detection and/or quantitation of the ternary complex formed between solid-phase antibody, antigen, and 20 labeled antibody.

Typical, and preferred, immunometric assays include "forward" assays in which the antibody bound to the solid phase is first contacted with the sample being tested to extract the antigen form the sample by formation of a binary solid phase antibody-antigen 25 complex. After a suitable incubation period, the solid support or carrier is washed to remove the residue of the fluid sample, including unreacted antigen, if any, and then contacted with the solution containing an unknown quantity of labeled antibody (which functions as a "reporter molecule"). After a second incubation 30 period to permit the labeled antibody to complex with the antigen bound to the solid support or carrier through the unlabeled antibody, the solid support or carrier is washed a second time to remove the unreacted labeled antibody.

In another type of "sandwich" assay, which may also be 35 useful with the antigens of the present invention, the so-called "simultaneous" and "reverse" assays are used. A "simultaneous" and "reverse" assays are used. A simultaneous assay involves a single

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incubation step as the antibody bound to the solid support or carrier and labeled antibody are both added to the sample being tested at the same time. After the incubation is completed, the solid support or carrier is washed to remove the residue of fluid sample and uncomplexed labeled antibody. The presence of labeled antibody associated with the solid support or carrier is then determined as it would be in a conventional "forward" sandwich assay.

In the "reverse" assay, stepwise addition first of a solution of labeled antibody to the fluid sample followed by the addition of unlabeled antibody bound to a solid support or carrier after a suitable incubation period is utilized. After a second incubation, the solid phase is washed in conventional fashion to free it of the residue of the sample being tested and the solution of unreacted labeled antibody. The determination of labeled antibody associated with a solid support or carrier is then determined as in the "simultaneous" and "forward" assays. See, e.g., for the above-mentioned immunological techniques, Harlow, supra; Ausubel et al, supra; and Sambrook et al, supra. GPR polypeptides of the present invention can be made by chemical synthesis or by recombinant methods, wherein chemical synthesis is preferred.

Synthetic production of transmembrane proteins of the present invention

GPR polypeptides, variants and chemical derivatives thereof can be synthesized according to known method steps, including portions of known GPR transmembrane domains, consensus peptides thereof, conservative substitution derivative thereof or functional derivatives thereof.

Chemical polypeptide synthesis is a rapidly evolving area in the art, and methods of solid phase polypeptide synthesis are well-described in the following references, hereby entirely incorporated by reference: (Merrifield, B., *J. Amer. Chem. Soc.* 85:2149-2154 (1963); Merrifield, B., *Science* 232:341-347 (1986); Wade, J.D. et al., *Biopolymers* 25:S21-S37 (1986); Fields, G.B., *Int. J. Polypeptide Prot. Res.* 35:161 (1990); MilliGen Report Nos. 2 and 2a, Millipore Corporation, Bedford, MA, 1987) Ausubel et al, supra, and Sambrook et al. supra.

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In general, as is known in the art, such methods involve blocking or protecting reactive functional groups, such as free amino, carboxyl and thio groups. After polypeptide bond formation, the protective groups are removed (or de-protected). Thus, the
5 addition of each amino acid residue requires several reaction steps for protecting and deprotecting. Current methods utilize solid phase synthesis, wherein the C-terminal amino acid is covalently linked to an insoluble resin particle large enough to be separated from the fluid phase by filtration. Thus, reactants are removed by washing
10 the resin particles with appropriate solvents using an automated programmed machine. The completed polypeptide chain is cleaved from the resin by a reaction which does not affect polypeptide bonds.

In the more classical method, known as the "tBoc method," the amino group of the amino acid being added to the resin-bound
15 C-terminal amino acid is blocked with tert-butyloxycarbonyl chloride (tBoc). This protected amino acid is reacted with the bound amino acid in the presence of the condensing agent dicyclohexylcarbodiimide, allowing its carboxyl group to form a polypeptide bond the free amino group of the bound amino acid. The
20 amino-blocking group is then removed by acidification with trifluoroacetic acid (TFA); it subsequently decomposes into gaseous carbon dioxide and isobutylene. These steps are repeated cyclically for each additional amino acid residue. A more vigorous treatment with hydrogen fluoride (HF) or trifluoromethanesulfonyl derivatives
25 is common at the end of the synthesis to cleave the benzyl-derived side chain protecting groups and the polypeptide-resin bond.

More recently, the preferred "Fmoc" technique has been introduced as an alternative synthetic approach, offering milder reaction conditions, simpler activation procedures and compatibility
30 with continuous flow techniques. This method was used, e.g., to prepare the peptide sequences disclosed in the present application. Here, the α -amino group is protected by the base labile 9-fluorenylmethoxycarbonyl (Fmoc) group. The benzyl side chain protecting groups are replaced by the more acid labile t-butyl
35 derivatives. Repetitive acid treatments are replaced by deprotection with mild base solutions, e.g., 20% piperidine in dimethylformamide (DMF), and the final HF cleavage treatment is eliminated. A TFA

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solution is used instead to cleave side chain protecting groups and the polypeptide resin linkage simultaneously.

At least three different polypeptide-resin linkage agents can be used: substituted benzyl alcohol derivatives that can be
5 cleaved with 95% TFA to produce a polypeptide acid, methanolic ammonia to produce a polypeptide amide, or 1% TFA to produce a protected polypeptide which can then be used in fragment condensation procedures, as described by Atherton, E. et al., *J. Chem. Soc. Perkin Trans.* 1:538-546 (1981) and Sheppard, R.C. et al., *Int. J.*
10 *Polypeptide Prot. Res.* 20:451-454 (1982). Furthermore, highly reactive Fmoc amino acids are available as pentafluorophenyl esters or dihydro-oxobenzotriazine esters derivatives, saving the step of activation used in the tBoc method.

Sequences available to use as a basis for polypeptide
15 synthesis can be based on published sequences of G-protein coupled receptors, ligands and/or effectors, wherein the transmembrane or functional domains correspond to sections of hydrophobic or other amino acids of 5 to 100 amino acids, such as 5-10, 10-15, 15-25, 20-25, 23-27, 25-30, 28-35, 20-40, 10-40, 20-30, 30-40, 40-50, 10-80,
20 20-60 or 25-40 amino acids in length. Recombinant production of GPR polypeptides can be accomplished according to known method steps. Standard reference works setting forth the general principles of recombinant DNA technology include Watson, J.D. et al., *Molecular Biology of the Gene*, Volumes I and II, The Benjamin/Cummings
25 Publishing Company, Inc., publisher, Menlo Park, CA (1987); Darnell, J.E. et al., *Molecular Cell Biology*, Scientific American Books, Inc., publisher, New York, NY (1986); Lewin, B.M., *Genes III*, John Wiley & Sons, publishers, New York, NY (1989); Old, R.W., et al., *Principles of Gene Manipulation: An Introduction to Genetic*
30 *Engineering*, 2d edition, University of California Press, publisher, Berkeley, CA (1981); Ausubel et al, eds., *Current Protocols in Molecular Biology*, Wiley Interscience, publisher, New York, NY (1987, 1992); and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory, publisher, Cold
35 Spring Harbor, NY (1989), the entire contents of which references are herein incorporated by reference.

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A nucleic acid sequence encoding a GPR polypeptide of the present invention may be recombined with vector DNA in accordance with conventional techniques, including blunt-ended or staggered-ended termini for ligation, restriction enzyme digestion to provide appropriate termini, filling in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and ligation with appropriate ligases. Techniques for such manipulations are disclosed, e.g., by Ausubel et al, *supra*, and are well known in the art.

10 A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene expression as GPR polypeptides in recoverable amounts. The precise nature of the regulatory regions needed for gene expression may vary from organism to organism, as is well known in the analogous art.

15 See, e.g., Sambrook, *supra* and Ausubel *supra*.

The present invention accordingly encompasses the expression of a GPR polypeptide, in either prokaryotic or eukaryotic cells, although eukaryotic expression is preferred.

Preferred hosts are bacterial or eukaryotic hosts including bacteria, yeast, insects, fungi, bird and mammalian cells either *in vivo*, or *in situ*, or host cells of mammalian, insect, bird or yeast origin. It is preferred that the mammalian cell or tissue is of human, primate, hamster, rabbit, rodent, cow, pig, sheep, horse, goat, dog or cat origin, but any other mammalian cell may be used.

30 Further, by use of, for example, the yeast ubiquitin hydrolase system, *in vivo* synthesis of ubiquitin-transmembrane polypeptide fusion proteins may be accomplished. The fusion proteins so produced may be processed *in vivo* or purified and processed *in vitro*, allowing synthesis of a GPR polypeptide of the present invention with a specified amino terminus sequence. Moreover, problems associated with retention of initiation codon-derived methionine residues in direct yeast (or bacterial) expression may be

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avoided. Sabin et al., *Bio/Technol.* 7(7): 705-709 (1989); Miller et al., *Bio/Technol.* 7(7): 698-704 (1989).

Any of a series of yeast gene expression systems incorporating promoter and termination elements from the actively
5 expressed genes coding for glycolytic enzymes produced in large quantities when yeast are grown in mediums rich in glucose can be utilized to obtain GPR polypeptides of the present invention. Known glycolytic genes can also provide very efficient transcriptional control signals. For example, the promoter and terminator signals
10 of the phosphoglycerate kinase gene can be utilized.

Production of GPR polypeptides or functional derivatives thereof in insects can be achieved, for example, by infecting the insect host with a baculovirus engineered to express transmembrane polypeptide by methods known to those of skill. See Ausubel et al,
15 eds. *Current Protocols in Molecular Biology*, Wiley Interscience, §§16.8-16.11 (1987, 1992).

In a preferred embodiment, the introduced nucleotide sequence will be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide
20 variety of vectors may be employed for this purpose. See, e.g., Ausubel et al, supra, §§ 1.5, 1.10, 7.1, 7.3, 8.1, 9.6, 9.7, 13.4, 16.2, 16.6, and 16.8-16.11. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and
25 selected from those recipient cells which do not contain the vector; the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors known in the art include
30 plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColE1, pSC101, pACYC 184, π VX). Such plasmids are, for example, disclosed by Maniatis, T., et al. (*Molecular Cloning, A Laboratory Manual*, Second Edition, Cold Spring Harbor Press, Cold Spring Harbor, NY (1989); Ausubel et al, eds., *Current*
35 *Protocols in Molecular Biology*, Wiley Interscience, New York, NY (1987, 1992)). *Bacillus* plasmids include pC194, pC221, pT127, etc. Such plasmids are disclosed by Gryczan, T. (In: *The Molecular*

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Biology of the Bacilli, Academic Press, NY (1982), pp. 307-329). Suitable *Streptomyces* plasmids include pIJ101 (Kendall, K.J., et al., *J. Bacteriol.* 169:4177-4183 (1987)), and streptomyces bacteriophages such as ϕ C31 (Chater, K.F., et al., In: *Sixth International Symposium on Actinomycetales Biology*, Akademiai Kiado, Budapest, Hungary (1986), pp. 45-54). *Pseudomonas* plasmids are reviewed by John, J.F., et al. (*Rev. Infect. Dis.* 8:693-704 (1986)), and Izaki, K. (*Jpn. J. Bacteriol.* 33:729-742 (1978); and Ausubel et al, *supra*).

The expressed protein may be isolated and purified in accordance with conventional conditions, such as extraction, precipitation, chromatography, affinity chromatography, electrophoresis, or the like. For example, the cells may be collected by centrifugation, or with suitable buffers, lysed, and the protein isolated by column chromatography, for example, on DEAE-cellulose, phosphocellulose, polyribocytidylic acid-agarose, hydroxyapatite or by electrophoresis or immunoprecipitation. Alternatively, the transmembrane polypeptide or functional derivative thereof may be isolated by the use of anti-transmembrane polypeptide antibodies. Such antibodies may be obtained by well-known methods, some of which are mentioned below. These antibodies may be immobilized on cellulose, agarose, hollow fibers, or cellulose filters by covalent chemical derivatives by methods well known to those skilled in the art.

As discussed herein, GPR polypeptides of the present invention may be further modified for purposes of drug design, such as for example to reduce immunogenicity, to prevent solubility and/or enhance delivery, or to prevent clearance or degradation.

Appropriate modification of the primary amino acid sequence of GPR polypeptides of the present invention, obtained by mutagenesis or utilizing fragments of other related forms of G-protein transmembrane proteins, as described herein, will allow the creation of molecules which bind G-protein coupled receptors with higher affinity than that exhibited by naturally occurring transmembrane domains. Small polypeptides that are provided according to the present invention which polypeptides maintain G-protein coupled receptor binding inhibition activity, are expected to have two

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advantages over larger polypeptides. These advantages include (1) greater stability and diffusibility, and (2) less immunogenicity.

Since polypeptides according to the present invention are generally small (10-40, 20-30, 15-25, 30-45 amino acids), cell or tissue sources of G-protein coupled receptors are not required to practice the present invention, since known polypeptide syntheses steps can be used without undue experimentation to provide GPR polypeptides or sequences substantially corresponding thereto.

Pharmaceutical Preparations

Preparations of GPR polypeptides for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions, which may contain auxiliary agents or excipients which are known in the art. Pharmaceutical compositions such as tablets and capsules can also be prepared according to routine methods.

By the term "protection" from infection or disease as used herein is intended "prevention," "suppression" or "treatment." "Prevention" involves administration of a GPR polypeptide, polypeptide derivative, or anti-idiotypic antibody prior to the induction of the disease.

"Suppression" involves administration of the composition prior to the clinical appearance of the disease.

"Treatment" involves administration of the protective composition after the appearance of the disease. It will be understood that in human and veterinary medicine, it is not always possible to distinguish between "preventing" and "suppressing" since the ultimate inductive event or events may be unknown, latent, or the patient is not ascertained until well after the occurrence of the event or events. Therefore, it is common to use the term "prophylaxis" as distinct from "treatment" to encompass both "preventing" and "suppressing" as defined herein. The term "protection," as used herein, is meant to include "prophylaxis."

At least one GPR polypeptide, antibody or anti-idiotypic antibody of the present invention may be administered by any means that achieve their intended purpose, for example, to treat GPR related pathologies, such as psychotic disorders, including schizophrenia, by inhibition of binding of Dopamine D₂ receptors

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using a GPR polypeptide corresponding to a fragment or consensus portion of a dopamine D₂ transmembrane domain; in the form of a pharmaceutical composition.

For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, or buccal routes. Alternatively, or concurrently, administration may be by the oral route. Parenteral administration can be by bolus injection or by gradual perfusion over time.

10 A preferred mode of using a GPR pharmaceutical composition of the present invention is by intravenous or parenteral application.

A typical regimen for preventing, suppressing, or treating G-protein coupled receptor pathologies, such as dopamine receptor related schizophrenia, comprises administration of an effective
15 amount of a GPR polypeptide, consensus sequence, or chemical derivative thereof, administered over a period of one or several days, up to and including between one week and about 24 months.

It is understood that the dosage of a GPR polypeptide of the present invention administered *in vivo* or *in vitro* will be
20 dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. The ranges of effective doses provided below are not intended to limit the inventors and represent preferred dose ranges. However, the most preferred dosage will be tailored to
25 the individual subject, as is understood and determinable by one of skill in the art, without undue experimentation.

The total dose required for each treatment may be administered by multiple doses or in a single dose. a GPR polypeptide or functional a chemical derivative thereof may be
30 administered alone or in conjunction with other therapeutics directed to GPR related pathologies, such as a the dopamine receptor related pathology as a non limiting example, or directed to other symptoms of the disease.

Effective amounts of the a GPR polypeptide or composition,
35 which may also include a functional derivative thereof, or a GPR anti-idiotypic antibody, are from about 0.01 μ g to about 100 mg/kg body weight, and preferably from about 10 μ g to about 50 mg/kg body

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weight, such 0.05, 0.07, 0.09, 0.1, 0.5, 0.7, 0.9, 1, 2, 5, 10, 20, 25, 30, 40, 45, or 50 mg/kg.

Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions, which
5 may contain auxiliary agents or excipients which are known in the art. Pharmaceutical compositions such as tablets and capsules can also be prepared according to routine methods.

Pharmaceutical compositions comprising at least one GPR polypeptide of the present invention may
10 include all compositions wherein the GPR polypeptide is contained in an amount effective to achieve its intended purpose. In addition to the GPR polypeptide, a pharmaceutical composition may contain suitable pharmaceutically acceptable carriers, such as comprising excipients and auxiliaries which facilitate processing of the active
15 compounds into preparations which can be used pharmaceutically.

Pharmaceutical compositions include suitable solutions for administration intravenously, subcutaneously, dermally, orally, mucosally, rectally or may by injection or orally, and contain from about 0.01 to 99 percent, preferably from about 20 to 75 percent of
20 active component (i.e. the antibody) together with the excipient. Pharmaceutical compositions for oral administration include tablets and capsules. Compositions which can be administered rectally include suppositories.

25 Example 1: Synthesis of a G-Protein Transmembrane Polypeptide and Consensus Polypeptide

The polypeptides in Figs. 1-5 were synthesized using the following procedure and include the following characteristics.

Peptide I (SEQ ID NO:1), as shown in Fig. 1, was used as a control for hydrophobic interaction alone as the mechanism of binding
30 and was run in parallel with the test polypeptides described below. Polypeptide II (SEQ ID NO:2), as shown in Fig. 2, represents a membrane-spanning fragment of transmembrane segment III in the dopamine D₂ receptor. This particular fragment was chosen since it has been implicated in the β -adrenergic receptor as having many
35 residues which are involved in ligand binding interaction.

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Polypeptide III (SEQ ID NO:3), as shown in Fig. 3, represents the consensus polypeptide which was developed as a model for the dopamine D₂ system and polypeptide IV (SEQ ID NO:4), as shown in Fig. 4, is a control for length dependence to show how critical the polypeptide length is in binding studies. Polypeptide V (SEQ ID NO:5), as shown in Fig. 5, is a consensus sequence of transmembrane domains of dopamine receptors D₁ and D₂.

The above polypeptides I-V (SEQ ID NOS:1-5), as shown in Figs. 1-5, respectively, were synthesized using solid phase synthesis on a Milligen 9600 polypeptide synthesizer using Fmoc amino acids (provided by Milligen/Bioscience) and PAL polystyrene resin (Milligen/Bioscience). Coupling times were 1 hour and the polypeptides were cleaved by trifluoroacetic acid/phenol/H₂O/thioanisole/ethanedithiol (82.5:5:5:5:2.5) at room temperature for 2 hours. The filtrate was collected and washed with 2 mL of trifluoroacetic acid (TFA) and 1 mL of dichloromethane (DCM). The filtrate was reduced in vacuo to 2 mL in volume and the resulting polypeptide was precipitated out by the addition of water. The polypeptides were then dissolved in 1,1,1,3,3,3-hexafluoro-2-propanol [(HFIP) Eastman]; lyophilized; and stored at -20°C until purification. Polypeptides I-V (SEQ ID NOS:1-5), were purified using reverse-phase HPLC using a preparative Vydac C4 column (Vydac) at 60°C at a flow rate of 6.0 mL/min with a linear gradient of 0-100% B in a 60 min period at a UV detection wavelength of 275 nm.

Due to the highly hydrophobic nature of these polypeptides, methanol was used with 0.1% (W/V) TFA and 0.5% (W/V) HFIP as solvent A and 2-propanol with 0.1% TFA as solvent B, in order to purify these polypeptides. Further purification was performed with an analytical C4 column (Vydac) with an isocratic gradient of 40% B at a flow rate of 1 mL/min. Identity of the polypeptides was confirmed by Fast-atom bombardment mass spectrometry and electrospray mass spectrometry and amino acid analysis. Stock solutions of polypeptides were made in HFIP and stored at -20°- 80°C.

Circular Dichroism (CD). Spectra were recorded on an Aviv model 60 DS circular dichroism spectrophotometer at room temperature with a 1 cm by 1 mm cell. The amplitude of the CD signal was calibrated using 1 0.1% (w/v) solution of d (+)-camphorsulfonic acid

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(Aldrich) and the wavelength of the CD signal was set using standard absorbance peaks of benzene vapor. Polypeptide concentrations were determined in a Cary 210 UV spectrophotometer with the absorbance measured at 280 nm. Helical content was estimated using CD signal intensity according to the method of Chen. et al Biochem. 13:3350-3359 (1974). This calculation compares the experimental ellipticity at 222 nm ($[\theta]_{222}$) ($[\theta]$) to a theoretical $[\theta]_{222}$. The theoretical $[\theta]_{222}$ is empirically adjusted to account for differences in polypeptide length and is based on experimental CD data from a series of proteins with known crystal structures. Since both the curve shape and magnitude are important in analysis of a CD spectrum for secondary structure contributions, we also considered qualitatively the contributions to the spectral shapes from different secondary structures using reference curves for poly (L-lysine).

Fig. 6 shows a CD spectrum of the consensus polypeptide III (SEQ ID NO:3) demonstrating that the polypeptide III is only partially helical in a solvent system in which most membrane polypeptides are strongly helical.

Preparation of Small Unilamellar Vesicles. Polypeptides were incorporated into DMPC vesicles at lipid:peptide ratio of 147:1 in the following manner: polypeptide in HFIP was mixed with dimyrystyroyl- phosphatidylcholine (synthetic) (DMPC) in dry chloroform and dried to a film with a stream of dry nitrogen at 0°C. This residue was then dried further overnight under a vacuum (1×10^{-2} torr). The residue was then hydrated in 100 mM NaCl and sonicated for a 30-min period under nitrogen at 0°C. The suspension was sedimented for a 30-min at 100,000 g (4°C) to remove any residual titanium particles and large unilamellar vesicles. The supernatant was removed and sedimented once more at 159,000 g for a 45 min period at 4°C. The supernatant in the lower portion was used immediately. This basic procedure has been shown to reliably produce small unilamellar vesicles.

Radioligand Binding Assays. A 0.50 mL volume of 1.00 nM [^3H]-spiperone (New England specific activity 21.4 Ci/mmol) was added to assay tubes which contained 0.5 mL lipid/peptide supernatant, 0.5 mL Tris buffer pH 7.4 and 0.5 mL of cold drug for a final volume of 2.0 mL. Nonspecific binding was defined in the presence of 1 μM of

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(+) butaclamol or 1 μ M spiperone. Appropriate controls for lipid vesicles containing no polypeptide were also run. Assay tubes were prepared in triplicate and the mixture was incubated for 1 h at 25°C. Incubation was terminated by filtration through filters presoaked in
5 0.1% polyethyleneimine (w/v, Sigma) for at least 1 h prior to use.

Filters were then washed with 6.0 mL of cold 50 mM Tris-HCl buffer, pH 7.40. For detection of radioactivity, filters were placed in 2.0 mL of scintillation fluid (Scintiverse) and incubated for 24 h. The activity of the tritium was determined in a Beckman LS 7500
10 liquid scintillation counter. Specific binding of [3 H]-spiperone was defined as the difference in binding in the presence and absence of unlabeled (+) butaclamol.

Fig. 7 shows results of radioligand binding assays comparing polypeptide I (SEQ ID NO:1) as a control unit polypeptide
15 III (SEQ ID NO:3) according to the present invention. Polypeptide III (SEQ ID NO:3) is shown to unexpectedly provide receptor-like functional binding, as demonstrated by binding to the neuroleptic agent, spiperone, into a stereoselective, concentration-dependent manner.

20 It has also been demonstrated that as little as 0.1% of a GPR polypeptide according to the present invention is able to form a receptor-like functional binding site. Thus, a GPR polypeptide of the present invention is unexpectedly shown to act both as GPR ligands and GPR binding sites.

25 All references cited herein, including journal articles or abstracts, published or corresponding U.S. or foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited
30 references. Additionally, the contents of the references cited within the references cited herein are also entirely incorporated by reference.

Reference to known method steps, conventional methods steps, known methods or conventional methods is not in any way an
35 admission that any aspect, description or embodiment of the present invention is disclosed, taught or suggested in the relevant art.

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The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art (including the contents of the references cited herein), readily modify and/or adapt
5 for various applications such specific embodiments, without undue experimentation, without departing from the generic concept of the present invention. Therefore, such adaptations and modifications are intended to be comprehended within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and
10 guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance presented herein.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Murphy, Randall B.
Schuster, David I.
- 5 (ii) TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED RECEPTOR PROTEINS, AND
COMPOSITIONS AND METHODS THEREOF
- (iii) NUMBER OF SEQUENCES: 95
- (iv) CORRESPONDENCE ADDRESS:
- 10 (A) ADDRESSEE: BROWDY AND NEIMARK
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(E) COUNTRY: USA
(F) ZIP: 20004
- 15 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 20 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/943,236
(B) FILING DATE: 10-SEP-1992
(C) CLASSIFICATION:
- 25 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Townsend, Kevin G.
(B) REGISTRATION NUMBER: 34,033
(C) REFERENCE/DOCKET NUMBER: MURPHY=2
- (ix) TELECOMMUNICATION INFORMATION:
- 30 (A) TELEPHONE: 202-628-5197
(B) TELEFAX: 202-737-3528
(C) TELEX: 248633

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- 40 Leu Ser Leu Leu Leu Ser Leu Leu Ser Leu Leu Ser Leu Leu Ser
1 5 10 15
Leu Leu Leu Ser Leu Tyr Tyr Tyr
20

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Asp Asp Ile Phe Val Thr Leu Asp Val Leu Phe Ser Thr Ala Ser Ile
1 5 10 15
Leu Asn Leu Ser Ala Ile Ser Leu Lys Lys Lys
20 25
- 55

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Tyr Ala Ile Phe Val Leu Tyr Ala Ser Ala Trp Leu Ser Phe Asn
 1 5 10 15

Cys Pro Phe Ile Val Thr Leu Asn Ile Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Ala Val Val Tyr Ser Ser Ile Val Ser Phe Tyr Val Phe Ile Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Cys Asp Val Phe Val Phe Val Asp Ile Met Leu Cys Thr Ala Ser
 1 5 10 15

Ile Phe Asn Leu Cys Ala Ile Ser Val Gly Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Leu Val Leu Leu Leu Phe Ala Asp Phe Ser Ser Met Leu Gly Cys
 1 5 10 15

Met Ala Val Leu Ile Gly Phe Trp Arg Leu Lys Leu Leu Arg Asn His
 20 25 30

Val Thr Lys Val Ile Ala Cys Phe Cys Ala Thr Ser Phe Cys Lys Asp
 35 40 45

Phe Pro Ser Thr Ile Leu Thr Leu Thr Asn Thr Ala Val Asn Gly Gly
 50 55 60

Phe Pro Cys Tyr Leu Tyr Ala Ile Val Ile Thr Tyr Gly Ser Phe Ala
 65 70 75 80

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Cys Trp Leu Trp Thr Leu Ile Cys Leu Ala Ile Ser Ile Tyr Met Leu
 85 90 95
 Ile Val Lys Arg Glu Pro Glu Pro Glu Leu Phe Glu Lys Tyr Tyr Tyr
 100 105 110
 5 Leu Leu Cys Trp Gly Leu Pro Leu Ile Ser Thr Ile Gly Leu Lys Asn
 115 120 125
 Thr Val Gln Phe Val Gly Asn Trp Cys Trp Ile Gly Val Ser Phe Thr
 130 135 140
 10 Gly Tyr Arg Phe Gly Leu Phe Tyr Pro Phe Leu Phe Ile Trp Ala Ile
 145 150 155 160
 Ser Ala Val Leu Val Gly Leu Thr Ser Arg Tyr Thr Tyr Trp Ile His
 165 170 175
 Asn Gly Val Ser Asp Asn Lys Glu Lys His Leu Thr Tyr Gln Phe Lys
 180 185 190
 15 Leu Ile Asn Tyr Ile Ile Val Phe Leu Val Cys Trp Val Phe Ala Val
 195 200 205
 Val Asn Arg Ile Val Asn Gly Leu Asn Trp Pro Pro Ala Leu Asn Ile
 210 215 220
 20 Leu His Thr Tyr Leu Ser Val Ser His Gly Phe Trp Ala Ser Val Thr
 225 230 235 240
 Phe Ile Tyr Asn Asn Pro Leu Met Trp Arg Tyr Phe Gly Ala Lys Ile
 245 250 255
 Leu Thr Val Phe Thr Phe Phe Gly Tyr Phe Thr Asp Val Gln Lys Lys
 260 265 270
 25 Leu Glu Lys Asn Leu Ser Pro Tyr Ser Ser Ser Arg Gly Thr Ser Gly
 275 280 285
 Lys Thr Met Leu Gly His Pro Thr Gly Asp Asp Val Gln Cys Ser Ser
 290 295 300
 30 Asp Leu Gln Cys Ser Leu Glu Arg His Pro Asn Met Val
 305 310 315

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 349 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

40 Val Tyr Ile Thr Val Glu Leu Ala Ile Ala Val Leu Ala Thr Leu Gly
 1 5 10 15
 Asn Val Leu Val Cys Trp Ala Val Trp Leu Asn Ser Asn Leu Asn Val
 20 25 30
 Thr Asn Tyr Phe Val Val Ser Leu Ala Ala Ala Asp Ile Ala Val Gly
 35 40 45
 45 Val Ile Ala Ile Pro Phe Ala Ile Thr Ile Ser Thr Gly Phe Cys Ala
 50 55 60
 Ala Cys His Asn Cys Leu Phe Phe Ala Cys Phe Val Leu Val Leu Thr

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	65		70		75		80									
	Gln	Ser	Ser	Ile	Phe	Ser	Leu	Leu	Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Ile
					85					90					95	
5	Ala	Ile	Arg	Ile	Pro	Leu	Arg	Tyr	Asn	Gly	Leu	Val	Thr	Gly	Thr	Arg
				100					105					110		
	Ala	Lys	Gly	Ile	Ile	Ala	Val	Cys	Trp	Val	Leu	Ser	Phe	Ala	Ile	Gly
			115					120					125			
	Leu	Thr	Pro	Met	Leu	Gly	Trp	Asn	Asn	Cys	Ser	Gln	Pro	Lys	Glu	Gly
		130					135					140				
10	Arg	Asn	Tyr	Ser	Gln	Gly	Cys	Gly	Glu	Gly	Gln	Val	Ala	Cys	Leu	Phe
	145					150					155					160
	Glu	Asp	Val	Val	Pro	Met	Asn	Tyr	Met	Val	Tyr	Tyr	Asn	Phe	Phe	Ala
					165					170					175	
15	Phe	Val	Leu	Val	Pro	Leu	Leu	Leu	Val	Tyr	Leu	Arg	Ile	Phe	Leu	Ala
				180					185					190		
	Ala	Arg	Arg	Gln	Leu	Lys	Gln	Met	Glu	Ser	Gln	Pro	Leu	Pro	Gly	Glu
			195					200					205			
	Arg	Ala	Arg	Ser	Thr	Leu	Gln	Lys	Glu	Val	His	Ala	Ala	Lys	Ser	Ala
		210					215					220				
20	Ile	Ile	Val	Gly	Leu	Phe	Ala	Leu	Cys	Trp	Leu	Pro	Leu	His	Ile	Ile
	225					230					235				240	
	Asn	Cys	Phe	Thr	Phe	Phe	Cys	Pro	Glu	Cys	Ser	His	Ala	Pro	Leu	Trp
					245					250					255	
25	Leu	Met	Tyr	Leu	Thr	Ile	Val	Leu	Ser	His	Thr	Asn	Ser	Trp	Asn	Pro
				260					265					270		
	Phe	Ile	Tyr	Ala	Tyr	Arg	Ile	Arg	Glu	Phe	Arg	Gln	Thr	Phe	Arg	Lys
			275					280					285			
	Ile	Ile	Arg	Ser	His	Val	Leu	Arg	Arg	Arg	Glu	Pro	Phe	Lys	Ala	Gly
		290					295					300				
30	Gly	Thr	Ser	Ala	Arg	Ala	Leu	Ala	Ala	His	Gly	Ser	Asp	Gly	Glu	Gln
	305					310					315					320
	Ile	Ser	Leu	Arg	Leu	Asn	Gly	His	Pro	Pro	Gly	Val	Trp	Ala	Asn	Gly
					325					330					335	
35	Ser	Ala	Pro	His	Pro	Glu	Arg	Arg	Pro	Asn	Gly	Tyr	Thr			
				340					345							

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 314 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

45 Ala Tyr Ile Gly Ile Glu Val Leu Ile Ala Leu Val Ser Val Pro Gly
 1 5 10 15

Trp Leu Val Ile Trp Ala Val Lys Val Asn Gln Ala Leu Arg Asp Ala
 20 25 30

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Thr Phe Cys Phe Ile Val Ser Ile Ala Val Ala Asp Val Ala Val Gly
 35 40 45
 Ala Leu Val Ile Pro Leu Ala Ile Leu Ile Asn Ile Gly Pro Arg Thr
 50 55 60
 5 Tyr Phe His Thr Cys Leu Met Val Ala Cys Pro Val Leu Ile Leu Thr
 65 70 75 80
 Gln Ser Ser Ile Ile Ala Leu Leu Ala Ile Ala Val Asp Arg Tyr Leu
 85 90 95
 10 Arg Val Lys Ile Pro Leu Arg Tyr Lys Thr Val Val Thr Pro Arg Arg
 100 105 110
 Ala Ala Val Ala Ile Ala Gly Cys Trp Ile Leu Ser Phe Val Val Gly
 115 120 125
 Leu Thr Pro Leu Phe Gly Trp Asn Arg Leu Gly Glu Ala Gln Arg Ala
 130 135 140
 15 Trp Ala Ala Asn Gly Ser Gly Gly Glu Pro Val Ile Lys Cys Glu Phe
 145 150 155 160
 Glu Lys Val Ile Ser Met Glu Tyr Met Val Tyr Phe Asn Phe Phe Val
 165 170 175
 20 Trp Val Leu Pro Pro Leu Leu Leu Met Val Leu Ile Tyr Leu Glu Val
 180 185 190
 Phe Tyr Leu Ile Arg Arg Gln Leu Gly Lys Lys Val Ser Ala Ser Ser
 195 200 205
 Gly Asp Pro Gln Lys Tyr Tyr Gly Lys Glu Leu Lys Ile Ala Lys Ser
 210 215 220
 25 Leu Ala Leu Ile Leu Phe Leu Phe Ala Leu Ser Trp Leu Pro Leu His
 225 230 235 240
 Ile Ile Asn Cys Ile Thr Leu Phe Cys Pro Ser Cys Arg Lys Pro Ser
 245 250 255
 30 Ile Leu Met Tyr Ile Ala Ile Phe Leu Thr His Gly Asn Ser Ala Met
 260 265 270
 Pro Ile Val Tyr Ala Phe Arg Ile Gln Lys Phe Arg Val Thr Phe Leu
 275 280 285
 Lys Ile Trp Asn Asp His Phe Arg Cys Gln Pro Thr Pro Pro Val Asp
 290 295 300
 35 Glu Asp Pro Pro Glu Glu Ala Pro His Asp
 305 310

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45 Val Ala Phe Ile Gly Ile Thr Thr Gly Leu Leu Ser Ile Ala Thr Val
 1 5 10 15
 Thr Gly Asn Leu Leu Val Leu Ile Ser Phe Lys Val Asn Thr Glu Leu

- 60 -

	20	25	30
	Lys Thr Val Asn Asn Tyr Phe Leu Leu Ser Ile Ala Cys Ala Asp Leu 35 40 45		
5	Ile Ile Gly Thr Phe Ser Met Leu Tyr Leu Leu Met His Trp Ala Leu 50 55 60		
	Gly Thr Leu Ala Cys Asp Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser 65 70 75 80		
	Asn Ala Ser Val Leu Asn Leu Leu Leu Ile Ser Phe Asp Arg Tyr Phe 85 90 95		
10	Ser Val Thr Arg Pro Leu Ser Tyr Arg Ala Lys Arg Thr Pro Arg Arg 100 105 110		
	Ala Ala Ile Met Ile Gly Ile Ala Trp Leu Val Ser Phe Val Leu Trp 115 120 125		
15	Ala Pro Ala Ile Leu Phe Trp Gln Tyr Leu Val Gly Glu Arg Thr Met 130 135 140		
	Leu Ala Gly Gln Cys Tyr Ile Gln Phe Leu Ser Gln Pro Ile Ile Thr 145 150 155 160		
	Phe Gly Thr Ala Met Ala Ala Phe Tyr Met Pro Val Thr Val Met Thr 165 170 175		
20	Leu Tyr Trp Arg Ile Tyr Arg Phe Thr Glu Asn Arg Ala Arg Glu Leu 180 185 190		
	Gln Gly Ser Glu Thr Pro Gly Lys Gly Gly Gly Ser Ser Ser Ser Ser 195 200 205		
25	Glu Arg Ser Gln Pro Gly Ala Glu Gly Ser Pro Glu Thr Pro Lys Gly 210 215 220		
	Gln Lys Pro Arg Gly Lys Glu Leu Ala Lys Arg Lys Thr Phe Ser Leu 225 230 235 240		
	Val Lys Glu Lys Lys Ala Ala Arg Thr Leu Ser Ala Ile Leu Leu Ala 245 250 255		
30	Phe Ile Leu Thr Trp Thr Pro Tyr Asn Ile Met Val Leu Val Ser Thr 260 265 270		
	Phe Cys Lys Asp Cys Val Pro Glu Thr Leu Trp Glu Leu Gly Tyr Trp 275 280 285		
35	Leu Ile Cys Tyr Val Asn Ser Thr Ile Asn Pro Trp Tyr Ala Leu Cys 290 295 300		
	Asn Lys Ala Phe Arg Asp Thr Phe Arg Leu Leu Leu Leu Cys Trp Asp 305 310 315 320		
	Lys Arg Arg Trp Arg Lys Ile Pro Lys Arg Pro Gly Ser Val His Arg 325 330 335		
40	Thr Pro Ser Arg Gln Cys 340		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5	Val	Val	Phe	Ile	Val	Leu	Val	Ala	Gly	Ser	Leu	Ser	Leu	Val	Thr	Ile	1	5	10	15
	Ile	Gly	Asn	Ile	Leu	Val	Met	Val	Ser	Ile	Lys	Val	Asn	Arg	His	Tyr	20	25	30	
	Phe	Leu	Phe	Ser	Ile	Ala	Cys	Ala	Asp	Leu	Ile	Ile	Gly	Val	Phe	Ser	35	40	45	
10	Met	Asn	Leu	Tyr	Thr	Leu	Tyr	Thr	Val	Ile	Gly	Tyr	Trp	Pro	Leu	Gly	50	55	60	
	Pro	Val	Val	Cys	Asp	Leu	Tyr	Val	Val	Ser	Asn	Ala	Ser	Val	Met	Asn	65	70	75	80
15	Leu	Leu	Ile	Ile	Ser	Phe	Asp	Arg	Tyr	Phe	Cys	Val	Thr	Lys	Pro	Leu	85	90	95	
	Thr	Tyr	Pro	Val	Lys	Arg	Thr	Thr	Lys	Met	Ala	Gly	Met	Met	Ile	Ala	100	105	110	
	Ala	Ala	Trp	Val	Leu	Ser	Phe	Ile	Leu	Trp	Ala	Pro	Ala	Ile	Leu	Phe	115	120	125	
20	Trp	Gln	Phe	Ile	Val	Gly	Val	Arg	Thr	Val	Glu	Asp	Gly	Glu	Cys	Tyr	130	135	140	
	Ile	Gln	Phe	Phe	Ser	Asn	Pro	Ala	Val	Thr	Phe	Gly	Thr	Ala	Ile	Ala	145	150	155	160
25	Ala	Phe	Tyr	Leu	Pro	Val	Ile	Ile	Met	Ile	Val	Leu	Tyr	Trp	His	Ile	165	170	175	
	Ser	Arg	Ala	Ser	Lys	Ser	Arg	Ile	Lys	Lys	Asp	Lys	Lys	Glu	Pro	Val	180	185	190	
	Ala	Asn	Gln	Asp	Pro	Val	Ser	Pro	Ser	Leu	Val	Gln	Gly	Arg	Ile	Val	195	200	205	
30	Lys	Pro	Leu	Ser	Ser	Asp	Asp	Lys	Ile	Val	Arg	Arg	Thr	Lys	Gln	Pro	210	215	220	
	Ala	Lys	Lys	Lys	Pro	Pro	Pro	Ser	Arg	Glu	Lys	Lys	Val	Thr	Arg	Thr	225	230	235	240
35	Ile	Ala	Ile	Leu	Leu	Ala	Phe	Ile	Ile	Thr	Trp	Ala	Pro	Tyr	Asn	Val	245	250	255	
	Met	Val	Leu	Ile	Asn	Thr	Phe	Cys	Ala	Pro	Cys	Ile	Pro	Asn	Thr	Val	260	265	270	
	Trp	Arg	Ile	Gly	Tyr	Trp	Leu	Cys	Tyr	Ile	Asn	Ser	Thr	Ile	Asn	Pro	275	280	285	
40	Ala	Cys	Tyr	Ala	Leu	Cys	Asn	Ala	Thr	Phe	Lys	Lys	Thr	Phe	Lys	His	290	295	300	
	Leu	Ile	Met	Cys	His	Tyr	Lys	Asn	Ile	Gly	Ala	Thr	Arg				305	310	315	

(2) INFORMATION FOR SEQ ID NO:11:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
 Trp Phe Ile Ala Phe Leu Thr Gly Ile Leu Ala Leu Val Thr Ile Ile
 1 5 10 15
 Gly Asn Ile Leu Val Ile Val Ser Phe Lys Val Asn Lys Gln Leu Lys
 20 25 30
 10 Thr Val Asn Asn Tyr Phe Leu Leu Ser Leu Ala Cys Ala Asp Leu Ile
 35 40 45
 Ile Gly Val Ile Ser Met Asn Leu Phe Thr Thr Tyr Ile Ile Met Asn
 50 55 60
 15 Arg Trp Ala Leu Gly Asn Thr Ala Cys Asp Leu Trp Ile Ala Ile Asp
 65 70 75 80
 Tyr Val Ala Ser Asn Ala Ser Val Leu Asn Leu Leu Val Ile Ser Phe
 85 90 95
 Asp Arg Tyr Phe Ser Ile Thr Arg Pro Leu Thr Tyr Arg Ala Lys Arg
 100 105 110
 20 Thr Thr Lys Arg Ala Gly Val Met Ile Gly Leu Ala Trp Val Ile Ser
 115 120 125
 Phe Val Leu Trp Ala Pro Ala Ile Leu Phe Trp Gln Tyr Phe Val Gly
 130 135 140
 25 Lys Arg Thr Val Pro Pro Gly Glu Cys Phe Ile Gln Phe Leu Ser Glu
 145 150 155 160
 Pro Thr Ile Thr Phe Gly Thr Ala Ile Ala Ala Phe Tyr Met Pro Val
 165 170 175
 Thr Ile Met Arg Ile Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys
 180 185 190
 30 Arg Thr Lys Glu Leu Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu
 195 200 205
 Thr Glu Asn Phe Val His Pro Thr Gly Ser Ser Arg Ser Cys Ser Ser
 210 215 220
 35 Tyr Glu Leu Gln Gln Gln Lys Arg Phe Ala Leu Lys Thr Arg Ser Gln
 225 230 235 240
 Ile Thr Lys Arg Lys Leu Leu Val Lys Glu Lys Lys Ala Ala Gln Thr
 245 250 255
 Leu Ser Ala Ile Leu Leu Ala Phe Ile Ile Thr Trp Thr Pro Tyr Asn
 260 265 270
 40 Ile Met Val Leu Val Asn Thr Phe Cys Asp Ser Cys Ile Pro Lys Thr
 275 280 285
 Tyr Trp Asn Leu Gly Gly Tyr Trp Leu Cys Tyr Ile Asn Ser Thr Val
 290 295 300
 45 Asn Pro Val Cys Tyr Ala Leu Cys Asn Lys Thr Phe Arg Thr Thr Phe
 305 310 315 320
 Lys Thr Leu Leu Leu Cys Gln Cys Asp Lys Arg Lys Arg Arg Lys Gln

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325 330 335

Gln Tyr Gln Gln Arg Gln Ser Val Ile Phe His Lys Arg Val Pro Glu
340 345 350

5 Gln Ala Leu
355

(2) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Met Val Phe Ile Ala Thr Val Arg Gly Ser Leu Ser Leu Val Thr Val
1 5 10 15

Val Gly Asn Ile Leu Val Met Leu Ser Ile Lys Val Asn Arg Gln Leu
20 25 30

Gln Thr Val Asn Asn Tyr Phe Leu Phe Ser Ile Ala Cys Ala Asp Leu
35 40 45

20 Ile Ile Gly Ala Phe Ser Met Asn Leu Tyr Thr Val Tyr Ile Ile Lys
50 55 60

Gly Tyr Trp Pro Leu Gly Ala Trp Cys Asp Leu Trp Leu Ala Leu Asp
65 70 75 80

25 Tyr Val Val Ser Asn Ala Ser Val Met Leu Leu Ile Ile Ser Phe Asp
85 90 95

Arg Tyr Phe Cys Val Thr Lys Pro Leu Thr Tyr Pro Ala Arg Arg Thr
100 105 110

Thr Lys Met Ala Gly Ile Met Ile Ala Ala Ala Trp Val Leu Ser Phe
115 120 125

30 Val Leu Trp Ala Pro Ala Ile Leu Phe Trp Gln Phe Val Val Gly Lys
130 135 140

Arg Thr Val Pro Asp Asn Gln Cys Phe Ile Gln Phe Leu Ser Asn Pro
145 150 155 160

35 Ala Val Thr Phe Gly Thr Ala Ile Ala Ala Phe Tyr Leu Pro Val Val
165 170 175

Ile Met Ile Val Leu Tyr Ile His Ile Ser Leu Ala Ser Arg Ser Arg
180 185 190

Val His Lys His Arg Pro Glu Gly Pro Lys Glu Lys Lys Ala Lys Thr
195 200 205

40 Ile Ala Phe Leu Lys Ser Pro Ile Met Gln Ser Val Lys Lys Pro Pro
210 215 220

Pro Gly Glu Ala Lys Phe Ala Ser Ile Ala Arg Asn Gln Val Arg Lys
225 230 235 240

45 Lys Arg Gln Leu Ala Ala Arg Glu Arg Lys Val Thr Arg Thr Ile Phe
245 250 255

Ala Ile Leu Leu Ala Phe Ile Leu Thr Trp Thr Pro Tyr Asn Val Met
260 265 270

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Val Leu Val Asn Thr Phe Cys Gln Ser Cys Ile Pro Asp Thr Val Trp
 275 280 285
 Ser Ile Gly Tyr Trp Leu Ile Cys Tyr Val Asn Ser Thr Ile Asn Pro
 290 295 300
 5 Ala Cys Tyr Ala Leu Cys Asn Ala Thr Phe Lys Lys Thr Phe Arg His
 305 310 315 320
 Leu Leu Leu Cys Gln Arg Tyr Asn Ile Gly Thr Ala Arg
 325 330
 (2) INFORMATION FOR SEQ ID NO:13:
 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 15 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
 Val Ile Thr Ile Ala Val Val Thr Ala Val Val Ser Leu Met Thr Ile
 1 5 10 15
 20 Val Gly Asn Val Leu Val Met Ile Ser Phe Lys Val Asn Ser Gln Leu
 20 25 30
 Lys Thr Val Asn Asn Tyr Tyr Leu Leu Ser Ile Ala Cys Ala Asp Leu
 35 40 45
 Ile Ile Gly Ile Phe Ser Met Asn Leu Tyr Thr Thr Tyr Ile Leu Ile
 50 55 60
 25 Met Gly Arg Trp Ala Leu Gly Ser Leu Ala Cys Asp Leu Trp Leu Ala
 65 70 75 80
 Ile Asp Tyr Val Ala Ser Asn Ala Ser Val Leu Asn Leu Leu Val Ile
 85 90 95
 30 Ser Phe Asp Arg Tyr Phe Ser Ile Thr Arg Pro Leu Thr Tyr Arg Ala
 100 105 110
 Lys Arg Thr Pro Lys Arg Ala Gly Ile Met Ile Gly Ile Ala Trp Leu
 115 120 125
 Ile Ser Phe Ile Leu Trp Ala Pro Ala Ile Leu Cys Trp Gln Tyr Leu
 130 135 140
 35 Val Gly Lys Arg Thr Val Pro Ile Asp Glu Cys Gln Ile Gln Phe Leu
 145 150 155 160
 Ser Glu Pro Thr Ile Thr Phe Gly Thr Ala Ile Ala Ala Phe Tyr Ile
 165 170 175
 40 Pro Val Ser Ile Met Arg Ile Leu Tyr Cys Arg Ile Tyr Arg Glu Thr
 180 185 190
 Glu Lys Arg Thr Lys Asp Leu Ala Asp Leu Gln Gly Ser Asp Ser Val
 195 200 205
 Tyr Lys Ala Glu Lys Arg Lys Pro Ala His Arg Ala Leu Phe Arg Ser
 210 215 220
 45 Cys Leu Arg Cys Pro Arg Pro Thr Lys Gly Leu Asn Pro Asn Pro Ser
 225 230 235 240
 His Gln Met Thr Lys Arg Lys Arg Met Ser Leu Val Lys Glu Arg Lys

245

250

255

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Ala Gly Asp Cys Leu Ile Met Leu Ile Val Leu Leu Ile Val Ala
1 5 10 15
Gly Asn Val Leu Val Ile Val Ala Ile Ala Lys Thr Pro Arg Leu Gln
20 25 30
Thr Leu Thr Asn Leu Phe Ile Met Ser Ile Ala Ser Ala Asp Leu Val
35 40 45
Met Leu Leu Leu Val Val Pro Phe Cys Ala Thr Leu Val Val Trp Gly
50 55 60
Arg Trp Glu Tyr Gly Ser Phe Phe Cys Glu Leu Trp Thr Ser Val Asp
65 70 75 80
Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala Leu
85 90 95
Asp Arg Tyr Leu Ala Ile Thr Ser Pro Phe Arg Tyr Gln Ser Leu Leu
100 105 110
Thr Arg Ala Arg Ala Arg Gly Leu Val Cys Thr Val Trp Ala Ile Ser
115 120 125
Ala Leu Val Ser Phe Leu Pro Ile Leu Leu Ser Asp Glu Ala Arg Arg
130 135 140
Cys Tyr Asn Asp Pro Lys Cys Cys Asp Phe Val Thr Asn Arg Ala Tyr
145 150 155 160
Ala Ile Ala Ser Ser Val Val Ser Phe Tyr Val Pro Leu Cys Ile Met
165 170 175
Phe Val Tyr Leu Arg Val Phe Arg Glu Ala Gln Lys Gln Val Lys Lys
180 185 190
Ile Asp Ser Cys Glu Arg Arg Phe Leu Gly Gly Pro Ala Arg Pro Pro
195 200 205

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Ser Pro Ser Pro Ser Pro Val Pro Ala Pro Ala Pro Pro Gly Pro Pro
 210 215 220
 Arg Pro Ala Ala Ala Ala Ala Thr Ala Pro Leu Ala Asn Gly Arg Ala
 225 230 235 240
 5 Gly Lys Arg Arg Pro Ser Arg Leu Val Ala Leu Arg Glu Gln Lys Ala
 245 250 255
 Leu Lys Thr Leu Gly Ile Ile Met Gly Val Phe Thr Leu Cys Trp Leu
 260 265 270
 10 Pro Phe Phe His Arg Glu Leu Val Pro Asp Arg Leu Phe Val Phe Phe
 275 280 285
 Asn Trp Leu Arg Tyr Ala Asn Ser Ala Phe Asn Pro Ile Ile Tyr Cys
 290 295 300
 Arg Ser Pro Asp Phe Arg Lys Ala Phe Gln Gly Leu Leu Cys Cys Ala
 305 310 315 320
 15 Arg Arg Ala Ala Arg Arg Arg His Ala Thr His Gly Asp Arg Pro Arg
 325 330 335
 Ala Ser Gly Cys Ile Ala Arg Pro Gly Pro Pro Ser Pro Gly Ala Ala
 340 345 350
 20 Ser Asp Asp Asp Asp Asp Val Val Gly Ala Thr Pro Pro Ala Arg
 355 360 365
 Leu Leu Glu Pro Trp Ala Gly Cys Asn
 370 375

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30 Val Val Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val Phe Gly
 1 5 10 15
 Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu Gln Thr
 20 25 30
 35 Val Thr Asn Tyr Phe Ile Thr Ser Ile Ala Cys Ala Asp Leu Val Met
 35 40 45
 Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met Lys Met
 50 55 60
 40 Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile Asp Val
 65 70 75 80
 Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala Val Asp
 85 90 95
 Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu Leu Thr
 100 105 110
 45 Lys Asn Lys Ala Arg Val Ile Ile Ile Met Val Trp Ile Val Ser Gly
 115 120 125
 Leu Thr Ser Phe Leu Pro Ile Leu Tyr Arg Ala Thr His Gln Glu Ala

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	130		135		140
	Ile Asn Cys Tyr Ala	Asn Glu Thr Cys Cys Asp	Phe Phe Thr Asn Gln		
	145	150	155	160	
5	Ala Tyr Ala Ala Ser	Ser Ala Val Ser Phe Tyr	Val Pro Leu Val Ile		
	165	170	175		
	Met Val Phe Val Tyr	Ser Arg Val Phe Gln Glu	Ala Lys Arg Gln Leu		
	180	185	190		
	Gln Lys Ile Asp Lys	Ser Glu Gly Arg Phe	Ile Phe Val Gln Asn Leu		
	195	200	205		
10	Ser Gln Val Glu Gln	Asp Gly Arg Thr Gly	His Gly Leu Arg Arg Ser		
	210	215	220		
	Ser Lys Phe Cys Leu	Lys Glu His Lys Ala	Leu Lys Thr Leu Gly Ile		
	225	230	235	240	
15	Ile Pro Cys Thr Phe	Thr Leu Cys Trp Leu	Pro Phe Phe Ile Val Asn		
	245	250	255		
	Ile Val Val Ile Gln	Asp Asn Leu Ile Arg	Lys Glu Val Tyr Ile Leu		
	260	265	270		
	Leu Asn Trp Ile Gly	Tyr Val Asn Ser Gly	Phe Asn Pro Leu Ile Tyr		
	275	280	285		
20	Cys Arg Ser Pro Asp	Phe Arg Ile Ala Phe	Gln Glu Leu Leu Cys Leu		
	290	295	300		
	Arg Arg Ser Ser Leu	Lys Ala Tyr Gly Asn	Gly Tyr Ser Ser Asn Gly		
	305	310	315	320	
25	Asn Thr Gly Glu Gln	Ser Gly Tyr His Val	Glu Gln Glu Lys Glu Asn		
	325	330	335		
	Lys Leu Leu Cys Glu	Asp Leu Pro Gly Thr	Glu Asp Phe Val Gly His		
	340	345	350		
	Gln Gly Thr Val Pro	Ser Asp Asn Ile Asp			
	355	360			
30	(2) INFORMATION FOR SEQ ID NO:16:				
	(i) SEQUENCE CHARACTERISTICS:				
	(A) LENGTH: 362 amino acids				
	(B) TYPE: amino acid				
	(C) STRANDEDNESS: single				
35	(D) TOPOLOGY: linear				
	(ii) MOLECULE TYPE: peptide				
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:				
	Ala Ala Leu Ala Gly	Ala Leu Leu Ala Leu	Ala Val Leu Ala Thr Val		
	1	5	10	15	
40	Gly Gly Asn Leu Leu	Val Ile Val Ala Ile	Ala Trp Thr Pro Arg Leu		
	20	25	30		
	Gln Thr Met Thr Asn	Val Phe Val Thr Ser	Leu Ala Ala Asp Leu		
	35	40	45		
45	Asp Leu Leu Val Val	Pro Pro Ala Ala Thr	Leu Ala Leu Thr Gly His		
	50	55	60		
	Trp Pro Leu Gly Ala	Thr Gly Cys Glu Leu	Trp Thr Ser Val Asp Val		
	65	70	75	80	

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Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Ala Ile Ala Val Asp
 85 90 95
 Arg Tyr Leu Ala Val Thr Asn Pro Leu Arg Tyr Gly Ala Leu Val Thr
 100 105 110
 5 Lys Arg Cys Ala Arg Thr Ala Trp Leu Val Trp Val Val Ser Ala Ala
 115 120 125
 Val Ser Phe Ala Pro Ile Met Ser Gln Trp Trp Arg Val Gly Ala Asp
 130 135 140
 10 Ala Glu Ala Gln Arg Cys His Ser Asn Pro Arg Cys Cys Ala Phe Ala
 145 150 155 160
 Ser Asn Met Pro Tyr Ala Val Leu Leu Ser Ser Ser Val Ser Phe Tyr
 165 170 175
 Leu Pro Leu Leu Leu Phe Val Tyr Ala Arg Val Phe Trp Ala Thr Arg
 180 185 190
 15 Gln Leu Arg Leu Leu Arg Gly Glu Leu Gly Arg Phe Pro Pro Glu Glu
 195 200 205
 Ser Pro Pro Ala Pro Ser Arg Ser Leu Ala Pro Ala Pro Val Gly Thr
 210 215 220
 20 Gly Ala Pro Pro Glu Gly Val Pro Ala Cys Gly Arg Pro Pro Ala Arg
 225 230 235 240
 Leu Ile Pro Ile Arg Glu His Arg Ala Leu Cys Thr Leu Gly Leu Ile
 245 250 255
 Met Gly Thr Phe Thr Leu Cys Trp Leu Pro Phe Phe Ile Ala Asn Val
 260 265 270
 25 Leu Arg Ala Leu Gly Gly Pro Ser Leu Val Pro Gly Pro Ala Phe Leu
 275 280 285
 Ala Leu Asn Trp Leu Ile Gly Tyr Ala Asn Ser Ala Phe Asn Pro Leu
 290 295 300
 30 Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ser Ala Phe Arg Arg Leu Leu
 305 310 315 320
 Cys Arg Cys Gly Arg Arg Leu Pro Pro Glu Pro Cys Ala Ala Ala Arg
 325 330 335
 Pro Ala Leu Phe Pro Ser Gly Val Pro Ala Ala Glu Ser Ser Pro Ala
 340 345 350
 35 Gln Pro Arg Leu Cys Gln Arg Leu Asp Gly
 355 360

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

45 Ala Ile Leu Leu Gly Val Ile Leu Gly Gly Leu Ile Leu Phe Gly Val
 1 5 10 15
 Leu Gly Asn Ile Leu Val Ile Leu Ser Val Ala Cys His Arg His Leu

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	20	25	30
	His Ser Val Thr His Tyr Tyr Ile Val Asn Leu Ala Val Ala Asp Leu		
	35	40	45
5	Leu Leu Thr Ser Thr Val Leu Pro Phe Ser Ala Ile Phe Glu Ile Leu		
	50	55	60
	Gly Tyr Trp Lys Phe Gly Arg Val Phe Cys Asn Val Trp Ala Ala Val		
	65	70	75
	Asp Val Leu Cys Cys Thr Ala Ser Ile Met Leu Leu Cys Ile Ile Ser		
		85	90
10	Ile Asp Arg Tyr Ile Gly Val Ser Tyr Pro Leu Arg Tyr Pro Thr Ile		
	100	105	110
	Val Thr Gln Lys Arg Gly Leu Met Ala Leu Leu Cys Val Trp Ala Leu		
	115	120	125
15	Ser Leu Val Ile Ser Ile Gly Pro Leu Phe Gly Trp Arg Gln Pro Ala		
	130	135	140
	Pro Glu Asp Glu Thr Ile Cys Gln Ile Asn Glu Glu Pro Gly Tyr Val		
	145	150	155
	Leu Phe Ser Ala Leu Gly Ser Phe Tyr Val Pro Leu Thr Ile Ile Leu		
		165	170
20	Val Met Tyr Cys Arg Val Tyr Val Val Ala Lys Arg Glu Ser Arg Gly		
	180	185	190
	Leu Lys Ser Gly Leu Lys Thr Asp Lys Ser Asp Ser Glu Gln Val Thr		
	195	200	205
25	Leu Arg Ile His Arg Lys Asn Ala Gln Val Gly Gly Ser Gly Val Thr		
	210	215	220
	Ser Ala Lys Asn Lys Thr His Phe Ser Val Arg Leu Leu Lys Phe Ser		
	225	230	235
	Arg Glu Lys Lys Ala Ala Lys Thr Leu Gly Ile Val Val Gly Cys Phe		
		245	250
30	Val Leu Cys Trp Leu Pro Phe Phe Leu Val Met Pro Ile Gly Ser Phe		
	260	265	270
	Phe Pro Asp Phe Arg Pro Ser Glu Thr Val Phe Lys Ile Ala Phe Trp		
	275	280	285
35	Leu Gly Tyr Ile Asn Ser Cys Ile Asn Pro Ile Ile Tyr Pro Cys Ser		
	290	295	300
	Ser Gln Glu Phe Lys Lys Ala Phe Gln Asn Val Leu Arg Ile Gln Cys		
	305	310	315
	Leu Arg Arg Lys Gln Ser Ser Lys His Thr Leu Gly Tyr Thr Leu His		
		325	330
40	Ala Pro Ser His Val Leu Glu Gly Gln His Lys Asp Leu Val Arg Ile		
	340	345	350
	Pro Val Gly Ser Ala Glu Thr Phe Tyr Lys Ile Ser Lys Thr Asp Gly		
	355	360	365
45	Val Cys Glu Trp Lys Ile Phe		
	370	375	

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10 Ala Ile Ser Val Gly Leu Val Leu Gly Ala Phe Ile Leu Phe Ala Ile
 1 5 10 15
 Val Gly Asn Ile Leu Val Ile Leu Ser Val Ala Cys Asn Arg His Leu
 20 25 30
 Arg Thr Pro Thr Asn Tyr Phe Ile Val Asn Ile Ala Ile Ala Asp Leu
 35 40 45
 15 Leu Leu Ser Phe Thr Val Leu Pro Phe Ser Ala Thr Leu Glu Val Leu
 50 55 60
 Gly Tyr Trp Val Leu Gly Arg Ile Phe Cys Asp Ile Trp Ala Ala Val
 65 70 75 80
 20 Asp Val Leu Cys Cys Thr Ala Ser Ile Leu Ser Leu Cys Ala Ile Ser
 85 90 95
 Ile Asp Arg Tyr Ile Gly Val Arg Tyr Ser Leu Gln Tyr Pro Thr Leu
 100 105 110
 Val Thr Arg Arg Tyr Ala Ile Ile Ala Leu Leu Ser Val Trp Val Leu
 115 120 125
 25 Ser Thr Val Ile Ser Ile Gly Pro Leu Leu Gly Trp Lys Glu Pro Ala
 130 135 140
 Pro Asn Asp Asp Lys Glu Cys Val Thr Glu Glu Pro Phe Leu Phe Cys
 145 150 155 160
 30 Ser Leu Gly Ser Phe Tyr Ile Pro Ile Ala Val Ile Leu Val Met Tyr
 165 170 175
 Cys Arg Val Tyr Ile Val Ala Lys Arg Thr Thr Lys Asn Leu Glu Ala
 180 185 190
 Gly Val Met Lys Glu Met Ser Asn Ser Lys Phe Leu Thr Leu Arg Ile
 195 200 205
 35 His Trp Ser Lys Asn Phe His Glu Asp Thr Leu Ser Ser Thr Lys Ala
 210 215 220
 Lys Gly His Asn Pro Arg Ser Ser Ile Ala Val Lys Leu Phe Lys Phe
 225 230 235 240
 40 Ser Arg Glu Lys Lys Ala Ala Lys Thr Leu Gly Ile Val Val Gly Trp
 245 250 255
 Ile Leu Cys Trp Leu Pro Phe Phe Ile Ala Leu Pro Leu Gly Ser Leu
 260 265 270
 Phe Ser Thr Leu Lys Pro Pro Asp Ala Val Phe Lys Trp Phe Trp Leu
 275 280 285
 45 Gly Tyr Phe Asn Ser Cys Leu Asn Pro Ile Ile Tyr Pro Cys Ser Ser
 290 295 300
 Lys Glu Phe Lys Arg Ala Leu Leu Gly Cys Gln Cys Arg Gly Gly Arg

	305					310						315					320
	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Leu	Ala	Cys	Ala	Tyr	Thr	Tyr	Arg	Pro	
					325					330					335		
5	Trp	Thr	Arg	Gly	Gly	Ser	Leu	Glu	Arg	Ser	Gln	Ser	Arg	Lys	Asp	Ser	
				340					345					350			
	Ile	Asp	Asp	Ser	Gly	Ser	Cys	Met	Ser	Gly	Gln	Lys	Arg	Thr	Leu	Pro	
			355					360					365				
	Ser	Ala															
10	(2)	INFORMATION FOR SEQ ID NO:19:															
	(i)	SEQUENCE CHARACTERISTICS:															
		(A) LENGTH: 330 amino acids															
		(B) TYPE: amino acid															
		(C) STRANDEDNESS: single															
15		(D) TOPOLOGY: linear															
	(ii)	MOLECULE TYPE: peptide															
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:19:															
	Val	Ala	Gly	Leu	Ala	Ala	Val	Val	Gly	Phe	Leu	Ile	Val	Phe	Thr	Val	
	1				5					10					15		
20	Val	Gly	Asn	Val	Leu	Val	Val	Ile	Ala	Val	Leu	Thr	Ser	Arg	Ala	Leu	
				20					25					30			
	Arg	Ala	Pro	Gln	Asn	Leu	Phe	Leu	Val	Ser	Ile	Ala	Ser	Ala	Asp	Ile	
			35					40					45				
25	Leu	Val	Ala	Thr	Leu	Val	Met	Pro	Phe	Ser	Leu	Ala	Asn	Glu	Ile	Met	
		50					55					60					
	Tyr	Trp	Tyr	Phe	Gly	Gln	Val	Trp	Cys	Gly	Val	Tyr	Leu	Ala	Ile	Asp	
	65					70					75					80	
	Val	Leu	Phe	Cys	Thr	Ser	Ser	Ile	Val	His	Leu	Cys	Ala	Ile	Ser	Leu	
					85					90					95		
30	Asp	Arg	Tyr	Trp	Ser	Val	Thr	Gln	Ala	Val	Glu	Tyr	Asn	Leu	Lys	Arg	
				100					105					110			
	Thr	Pro	Arg	Arg	Val	Lys	Ala	Thr	Ile	Val	Ala	Val	Trp	Leu	Ile	Ser	
			115					120					125				
35	Ala	Val	Ile	Ser	Phe	Pro	Pro	Leu	Val	Ser	Leu	Tyr	Arg	Gln	Pro	Asp	
		130					135					140					
	Gly	Ala	Ala	Tyr	Pro	Gln	Cys	Gly	Leu	Asn	Asp	Glu	Thr	Trp	Tyr	Ile	
	145					150					155					160	
	Leu	Ser	Ser	Cys	Ile	Gly	Ser	Phe	Phe	Ala	Pro	Cys	Leu	Ile	Tyr	Leu	
					165					170					175		
40	Leu	Val	Tyr	Ala	Arg	Ile	Tyr	Arg	Val	Ala	Lys	Arg	Arg	Thr	Arg	Thr	
				180					185					190			
	Leu	Ser	Glu	Lys	Arg	Ala	Pro	Val	Gly	Pro	Asp	Gly	Ala	Ser	Pro	Thr	
			195					200					205				
45	Thr	Glu	Asn	Gly	Leu	Gly	Ala	Ala	Ala	Gly	Glu	Ala	Arg	Thr	Gly	Thr	
		210					215					220					
	Ala	Arg	Phe	Leu	Ser	Arg	Arg	Arg	Arg	Ala	Arg	Ser	Ser				

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245 250 255
 Leu Val Phe Val Leu Cys Trp Phe Pro Phe Phe Phe Ile Tyr Ser Leu
 260 265 270
 5 Tyr Gly Ile Cys Arg Glu Ala Cys Gln Val Pro Gly Pro Leu Phe Lys
 275 280 285
 Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser Ser Leu Asn Pro Val Ile
 290 295 300
 Tyr Thr Val Phe Asn Gln Asp Phe Arg Pro Ser Phe Lys His Ile Leu
 305 310 315 320
 10 Phe Arg Arg Arg Arg Arg Gly Phe Arg Gln
 325 330

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
 20 Thr Ala Ala Ile Ala Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile
 1 5 10 15
 Phe Gly Asn Ala Leu Val Ile Ile Ala Val Leu Thr Ser Arg Ser Leu
 20 25 30
 25 Arg Ala Pro Gln Asn Leu Phe Leu Val Ser Ile Ala Ala Ala Asp Ile
 35 40 45
 Leu Val Ala Thr Leu Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu
 50 55 60
 Gly Tyr Trp Tyr Phe Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu
 65 70 75 80
 30 Asp Val Leu Phe Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser
 85 90 95
 Leu Asp Arg Tyr Trp Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys
 100 105 110
 35 Arg Thr Pro Arg Arg Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile
 115 120 125
 Ala Ala Val Ile Ser Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly
 130 135 140
 Pro Gln Pro Arg Gly Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp
 145 150 155 160
 40 Tyr Ile Leu Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Leu
 165 170 175
 Leu Val Tyr Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg
 180 185 190
 45 Gly Pro Arg Ala Lys Cys Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro
 195 200 205
 Arg Pro Asp His Gly Gly Ala Ile Ala Ser Ala Lys Leu Pro Ala Ile

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210 215 220

Ala Ser Gly Arg Gly Val Gly Ala Ile Gly Gly Gln Trp Trp Arg Arg
225 230 235 240

5 Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe Val Leu Ala Val
245 250 255

Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe Phe Phe Ser Tyr
260 265 270

Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val Pro His Gly Leu
275 280 285

10 Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser Ser Leu Asn Pro
290 295 300

Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Met Phe Arg Arg Ile
305 310 315 320

15 Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
325 330

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

25 Thr Leu Thr Leu Val Cys Ile Ala Cys Leu Ser Leu Thr Val Phe Gly
1 5 10 15

Asn Val Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala
20 25 30

Pro Gln Asn Leu Phe Leu Val Ser Ile Ala Ser Ala Asp Ile Leu Val
35 40 45

30 Ala Thr Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Asn Gly Tyr
50 55 60

Trp Tyr Phe Gly Lys Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu
65 70 75 80

35 Phe Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg
85 90 95

Tyr Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro
100 105 110

Arg Arg Ile Lys Ala Ile Ile Ile Thr Val Trp Val Ile Ser Ala Val
115 120 125

40 Ile Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Gly Gly Gly
130 135 140

Gly Pro Gln Pro Ala Glu Pro Arg Cys Glu Ile Asn Asp Gln Lys Trp
145 150 155 160

45 Tyr Val Ile Ser Ser Cys Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile
165 170 175

Trp Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg
180 185 190

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Val Pro Pro Ser Arg Arg Asp Pro Asp Ala Val Ala Ala Pro Pro Gly
 195 200 205
 Gly Thr Glu Arg Arg Pro Asn Gly Leu Gly Pro Glu Arg Ser Ala Gly
 210 215 220
 5 Pro Gly Gly Gly Arg Gly Arg Ser Ala Ser Gly Leu Pro Arg Arg Arg
 225 230 235 240
 Ala Gly Ala Gly Gly Gln Asn Arg Glu Lys Arg Phe Thr Phe Val Ile
 245 250 255
 10 Ala Val Val Ile Gly Val Phe Val Val Cys Trp Phe Pro Phe Phe
 260 265 270
 Thr Tyr Thr Leu Thr Ala Val Leu Cys Ser Val Pro Arg Thr Leu Phe
 275 280 285
 Lys Phe Phe Phe Trp Phe Gly Tyr Cys Asn Ser Ser Leu Asn Pro Val
 290 295 300
 15 Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala Phe Lys Lys Ile
 305 310 315 320
 Leu Cys Arg Gly Asp Arg Lys Arg Ile Val
 325 330
 (2) INFORMATION FOR SEQ ID NO:22:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 Thr Leu Thr Leu Val Cys Ile Ala Gly Leu Ile Met Leu Phe Thr Val
 1 5 10 15
 30 Phe Gly Asn Val Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu
 20 25 30
 Lys Ala Pro Gln Asn Leu Phe Leu Val Ser Ile Ala Ser Ala Asp Ile
 35 35 40 45
 Leu Val Ala Thr Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met
 50 55 60
 35 Tyr Trp Tyr Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Ile Asp
 65 70 75 80
 Val Leu Phe Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu
 85 90 95
 40 Asp Arg Tyr Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg
 100 105 110
 Thr Pro Arg Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser
 115 120 125
 Ala Val Ile Ser Phe Pro Pro Leu Leu Ile Ser Ile Glu Lys Lys Gly
 130 135 140
 45 Ala Gly Gly Gly Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp
 145 150 155 160
 Gln Lys Trp Tyr Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro

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	165	170	175
	Cys Leu Ile Asn His Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys 180 185 190		
5	Arg Arg Thr Arg Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Cys Ser 195 200 205		
	Ala Pro Pro Gly Gly Ala Asp Arg Arg Pro Asn Ala Val Gly Pro Glu 210 215 220		
	Arg Gly Ala Gly Thr Ala Gly Gly Gln Gly Glu Glu Arg Ala Gly Gly 225 230 235 240		
10	Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe 245 250 255		
	Thr Phe Val Ile Ala Val Val Ile Gly Val Phe Val Val Cys Trp Phe 260 265 270		
15	Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val Gly Cys Pro Val Pro 275 280 285		
	Tyr Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly Tyr Cys Asn Ser Ser 290 295 300		
	Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala 305 310 315 320		
20	Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg Ile Val 325 330		

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30	Leu Leu Thr Ala Leu Val Leu Ser Val Ile Ile Val Leu Thr Ile Ile 1 5 10 15
	Gly Asn Ile Leu Val Ile Leu Ser Val Phe Thr Tyr Lys Pro Leu Arg 20 25 30
35	Ile Val Gln Asn Phe Phe Ile Val Ser Ile Ala Val Ala Asp Leu Thr 35 40 45
	Val Ala Leu Leu Val Leu Pro Phe Trp Ala Tyr Ser Ile Leu Gly Arg 50 55 60
	Trp Glu Phe Gly Ile His Leu Cys Lys Leu Trp Leu Thr Cys Asp Val 65 70 75 80
40	Leu Cys Cys Thr Ser Ser Ile Leu Asn Leu Cys Ala Ile Ala Leu Asp 85 90 95
	Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asn Tyr Ala Gln Lys Arg Thr 100 105 110
45	Val Gly Arg Val Leu Leu Leu Ile Ser Gly Val Trp Leu Leu Ser Leu 115 120 125
	Leu Ile Ser Ser Pro Pro Leu Ile Gly Trp Asn Asp Trp Pro Asp Glu

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	130		135		140
	Phe Thr Ser Ala Thr	Pro Cys Glu Leu Thr	Ser Gln Arg Ile Gly Tyr		
	145	150	155	160	
5	Val Ile Tyr Ser Ser	Leu Gly Ser Phe Phe	Ile Pro Ile Ala Ile Met		
		165	170	175	
	Arg Ile Val Tyr Ile	Glu Ile Phe Val Ala Thr	Arg Arg Arg Leu Arg		
		180	185	190	
	Glu Arg Ala Arg Ala	Asn Lys Ile Asn Thr	Ile Ala Leu Lys Ser Thr		
		195	200	205	
10	Glu Leu Glu Pro Met	Ala Asn Ser Ser Pro	Val Ala Ala Ser Asn Ser		
		210	215	220	
	Gly Ser Lys Lys Lys	Thr Ser Gly Val Asn	Gln Phe Ile Glu Glu Lys		
		225	230	235	240
15	Gln Lys Ile Ser Leu	Ser Lys Glu Arg Arg	Ala Ala Arg Thr Leu Gly		
		245	250	255	
	Ile Ile Met Val Phe	Val Ile Cys Trp Leu	Pro Phe Phe Ile Met Tyr		
		260	265	270	
	Val Ile Leu Pro Phe	Cys Cys Pro Thr Asn	Lys Phe Lys Asn Phe Ile		
		275	280	285	
20	Thr Trp Leu Gly Tyr	Ile Asn Ser Gly Leu	Asn Pro Val Ile Tyr Thr		
		290	295	300	
	Ile Phe Asn Leu Asp	Tyr Arg Arg Ala Phe	Lys Arg Leu Leu Gly Leu		
		305	310	315	320
25	Asn				

(2) INFORMATION FOR SEQ ID NO:24:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 373 amino acids
30	(B) TYPE: amino acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
35	Arg Ile Leu Thr Ala Cys Phe Leu Ser Leu Leu Ile Leu Ser Thr Leu
	1 5 10 15
	Leu Gly Asn Thr Leu Val Cys Ala Ala Val Ile Arg Phe Arg His Leu
	20 25 30
	Arg Ser Lys Val Thr Asn Phe Phe Val Ile Ser Leu Ala Val Ser Asp
	35 40 45
40	Leu Leu Val Ala Val Leu Leu Trp Lys Ala Val Ala Glu Ile Ala Gly
	50 55 60
	Phe Trp Pro Phe Gly Ser Phe Cys Asn Ile Trp Val Ala Phe Asp Ile
	65 70 75 80
45	Met Cys Ser Thr Ala Ser Ile Leu Asn Leu Cys Val Ile Ser Val Asp
	85 90 95
	Arg Tyr Trp Ala Ile Ser Ser Pro Phe Arg Tyr Glu Arg Lys Lys Arg

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	100	105	110
	Pro Lys Ala Ala Phe Ile Leu Ile Ser Val Ala Trp Thr Leu Ser Val		
	115	120	125
5	Leu Ile Ser Phe Ile Pro Val Gln Leu Ser Trp His Lys Ala Lys Pro		
	130	135	140
	Thr Ser Pro Ser Asp Gly Met Ala Thr Ser Leu Ala Glu Thr Ile Asp		
	145	150	155
	Asn Cys Asp Ser Ser Leu Ser Arg Thr Tyr Ala Ile Ser Ser Ser Val		
	165	170	175
10	Ile Ser Phe Tyr Ile Pro Val Ala Ile Leu Val Thr Tyr Thr Arg Ile		
	180	185	190
	Tyr Arg Ile Ala Gln Lys Gln Ile Arg Arg Ile Ala Ala Leu Glu Arg		
	195	200	205
15	Ala Ala Val His Ala Lys Asn Cys Gln Gly Asn Lys Pro Val Glu Cys		
	210	215	220
	Ser Gln Pro Glu Ser Ser Phe Met Ser Phe Lys Arg Glu Thr Lys Val		
	225	230	235
	Leu Lys Thr Leu Ser Val Ile Thr Cys Val Phe Val Cys Cys Trp Leu		
	245	250	255
20	Pro Phe Phe Ile Leu Asn Cys Ile Leu Pro Phe Cys Gly Ser Gly Glu		
	260	265	270
	Thr Gln Pro Phe Cys Thr Asp Ser Asn Thr Phe Asp Val Phe Val Trp		
	275	280	285
25	Phe Gly Trp Ala Asn Ser Ser Leu Asn Pro Ile Ile Tyr Ala Phe Asn		
	290	295	300
	Ala Asp Phe Arg Lys Ala Phe Ser Thr Leu Leu Gly Cys Tyr Arg Leu		
	305	310	315
	Cys Pro Ala Thr Asn Met Ala Ile Glu Thr Val Ser Ile Asn Asn Gly		
	325	330	335
30	Ala Ala Met Phe Ser Ser His His Glu Pro Arg Gly Ser Ile Ser Lys		
	340	345	350
	Glu Cys Asn Leu Val Tyr Leu Ile Pro His Ala Val Gly Ser Ser Glu		
	355	360	365
35	Asp Leu Lys Lys Glu		
	370		
(2)	INFORMATION FOR SEQ ID NO:25:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 360 amino acids		
	(B) TYPE: amino acid		
40	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: peptide		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:		
45	Gln Trp Thr Ala Cys Leu Leu Thr Leu Leu Ile Ile Trp Thr Leu Leu		
	1	5	10
	Gly Asn Val Leu Val Cys Ala Ala Ile Val Arg Ser Arg His Leu Leu		
	20	25	30

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Val Phe Ile Val Ser Ile Ala Val Ser Asp Leu Phe Val Ala Leu Leu
 35 40 45
 Val Asn Thr Trp Lys Ala Tyr Ala Glu Val Ala Gly Tyr Trp Pro Phe
 50 55 60
 5 Gly Ala Phe Cys Asp Val Trp Val Ala Phe Asp Ile Met Cys Ser Thr
 65 70 75 80
 Ala Ser Ile Leu Asn Leu Cys Val Ile Ser Val Asp Arg Tyr Trp Ala
 85 90 95
 10 Ile Ser Arg Pro Phe Arg Tyr Lys Ala Leu Val Met Val Gly Ile Ala
 100 105 110
 Trp Thr Leu Ser Ile Leu Ile Ser Phe Ile Pro Val Gln Ile Asn Trp
 115 120 125
 Asn Arg Asp Gln Ala Ala Ser Trp Gly Gly Leu Asp Leu Pro Asn Asn
 130 135 140
 15 Ile Asp Cys Asp Ser Ser Leu Asn Arg Thr Tyr Ala Ile Ser Ser Ser
 145 150 155 160
 Leu Ile Ser Phe Tyr Ile Pro Val Ala Ile Leu Val Thr Tyr Thr Arg
 165 170 175
 20 Ile Tyr Arg Ile Ala Gln Val Gln Ile Arg Arg Ile Ser Ser Leu Glu
 180 185 190
 Arg Ala Ala Glu His Ala Gln Ser Cys Arg Ser Ser Ala Ala Cys Ala
 195 200 205
 Pro Asp Thr Ser Leu Arg Ala Ser Ile Lys Lys Glu Thr Lys Val Leu
 210 215 220
 25 Lys Thr Leu Ser Val Ile Ile Cys Val Phe Val Cys Cys Trp Leu Pro
 225 230 235 240
 Phe Phe Ile Leu Asn Cys Met Val Pro Phe Cys Ser Gly His Pro Glu
 245 250 255
 30 Gly Pro Pro Ala Gly Phe Pro Cys Val Ser Glu Thr Thr Phe Asp Val
 260 265 270
 Phe Val Trp Phe Gly Trp Ala Asn Ser Ser Leu Asn Pro Val Ile Tyr
 275 280 285
 Ala Phe Asn Ala Asp Phe Gln Lys Val Phe Ala Gln Leu Leu Cys Ser
 290 295 300
 35 His Phe Cys Ser Arg Thr Pro Val Glu Thr Val Asn Ile Ser Asn Glu
 305 310 315 320
 Leu Ile Ser Tyr Asn Gln Asp Ile Val Phe His Lys Glu Ile Ala Ala
 325 330 335
 40 Ala Tyr Ile His Met Met Pro Asn Ala Val Thr Pro Gly Asn Arg Glu
 340 345 350
 Val Asp Asn Asp Glu Glu Glu Gly
 355 360

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 314 amino acids
 (B) TYPE: amino acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5 Tyr Asn Tyr Tyr Ala Thr Leu Leu Thr Leu Leu Ile Ala Val Ile Val
 1 5 10 15
 Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala Leu
 20 25 30
 10 Gln Thr Met Asn Tyr Leu Ile Val Ser Ile Ala Val Ala Asp Leu Leu
 35 40 45
 Val Ala Thr Leu Val Trp Trp Trp Tyr Leu Glu Val Val Gly Glu Trp
 50 55 60
 Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr Leu Asp Ile Thr
 65 70 75 80
 15 Ala Ser Ile Leu Asn Leu Cys Ala Ile Ser Ile Asp Arg Tyr Thr Ala
 85 90 95
 Val Ala Met Pro Met Leu Tyr Asn Thr Arg Tyr Ser Ser Lys Arg Arg
 100 105 110
 20 Val Thr Val Met Ile Ser Ile Val Trp Val Leu Ser Phe Thr Ile Ser
 115 120 125
 Cys Pro Leu Leu Phe Gly Leu Asn Asn Ala Asp Gln Asn Glu Cys Ile
 130 135 140
 Ile Ala Asn Pro Ala Phe Val Val Tyr Ser Ser Ile Val Ser Phe Tyr
 145 150 155 160
 25 Val Pro Phe Ile Val Thr Leu Leu Val Tyr Ile Lys Ile Tyr Ile Val
 165 170 175
 Leu Arg Arg Arg Arg Lys Arg Val Asn Thr Lys Arg Ser Ser Arg Ala
 180 185 190
 30 Phe Arg Ala His Leu Arg Ala Pro Leu Lys Gly Asn Cys Thr His Pro
 195 200 205
 Glu Asp Met Lys Leu Cys Thr Val Ile Pro Asn Gly Lys Thr Arg Thr
 210 215 220
 Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu Lys
 225 230 235 240
 35 Lys Ala Thr Gln Met Ile Ala Ile Val Leu Gly Val Phe Ile Ile Cys
 245 250 255
 Lys Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp Cys
 260 265 270
 40 Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr Val
 275 280 285
 Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe
 290 295 300
 Arg Lys Ala Phe Leu Lys Ile Leu His Cys
 305 310

45 (2) INFORMATION FOR SEQ ID NO:27:
 (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

	Ala	Tyr	Tyr	Ala	Leu	Ser	Tyr	Cys	Ala	Leu	Ile	Leu	Ala	Ile	Val	Phe	
	1				5					10					15		
10	Gly	Asn	Gly	Leu	Val	Cys	Met	Ala	Val	Leu	Arg	Glu	Lys	Ala	Leu	Gln	
				20					25					30			
	Thr	Thr	Thr	Asn	Tyr	Leu	Val	Val	Ser	Leu	Ala	Val	Ala	Asp	Leu	Leu	
				35					40					45			
	Val	Ala	Thr	Leu	Val	Trp	Trp	Val	Val	Tyr	Leu	Glu	Val	Thr	Gly	Gly	
				50			55					60					
15	Val	Trp	Asn	Phe	Ser	Arg	Ile	Cys	Cys	Asp	Val	Phe	Val	Thr	Leu	Asp	
	65					70					75					80	
	Val	Met	Met	Thr	Ala	Ser	Ile	Leu	Asn	Leu	Cys	Ala	Ile	Ser	Ile	Asp	
					85					90					95		
20	Arg	Tyr	Thr	Ala	Val	His	Tyr	Gln	His	Gly	Thr	Gly	Gln	Ser	Ser	Cys	
				100					105					110			
	Arg	Arg	Val	Ala	Ile	Met	Ile	Thr	Ala	Val	Trp	Val	Leu	Ala	Phe	Ala	
				115				120					125				
	Val	Ser	Cys	Pro	Leu	Leu	Phe	Gly	Phe	Asn	Thr	Gly	Asp	Pro	Thr	Val	
				130			135					140					
25	Cys	Ser	Ile	Ser	Asn	Pro	Asp	Phe	Val	Ile	Tyr	Ser	Ser	Val	Val	Ser	
	145					150					155					160	
	Phe	Tyr	Leu	Pro	Phe	Gly	Val	Thr	Val	Leu	Val	Tyr	Ala	Arg	Ile	Tyr	
					165					170					175		
30	Val	Val	Leu	Lys	Gln	Arg	Arg	Arg	Lys	Arg	Ile	Leu	Thr	Arg	Gln	Asn	
				180					185					190			
	Ser	Gln	Cys	Asn	Ser	Val	Arg	Pro	Gly	Phe	Pro	Gln	Gln	Ser	Thr	Ser	
				195				200					205				
	Leu	Pro	Asp	Pro	Ala	His	Leu	Glu	Leu	Lys	Arg	Ser	Asn	Gly	Arg	Leu	
		210					215					220					
35	Ser	Thr	Ser	Leu	Lys	Leu	Pro	Leu	Gln	Pro	Arg	Gly	Val	Pro	Leu	Arg	
		225				230					235					240	
	Glu	Lys	Lys	Ala	Thr	Gln	Met	Val	Ala	Ile	Val	Leu	Gly	Ala	Phe	Ile	
					245					250					255		
40	Val	Cys	Trp	Leu	Pro	Phe	Phe	Leu	Thr	His	Val	Ile	Asn	Thr	His	Cys	
				260					265					270			
	Gln	Thr	Cys	His	Val	Ser	Pro	Glu	Leu	Tyr	Ser	Ala	Thr	Thr	Trp	Leu	
			275					280					285				
	Gly	Tyr	Val	Asn	Ser	Ala	Leu	Asn	Pro	Val	Ile	Tyr	Thr	Thr	Phe	Asn	
		290					295					300					
45	Ile	Glu	Phe	Arg	Lys	Ala	Phe	Leu	Leu	Ile	Leu	Ser	Cys				
	305					310					315						

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(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

10	Gly	Ala	Ala	Ala	Leu	Val	Gly	Gly	Val	Leu	Ile	Cys	Ala	Val	Leu
	1				5				10					15	
	Ala	Gly	Asn	Ser	Leu	Val	Cys	Val	Ser	Val	Ala	Thr	Glu	Arg	Ala
				20					25					30	Leu
	Gln	Thr	Pro	Thr	Asn	Ser	Phe	Ile	Val	Ser	Leu	Ala	Ala	Ala	Asp
			35				40						45		Leu
15	Leu	Leu	Ala	Leu	Leu	Val	Leu	Pro	Leu	Phe	Val	Tyr	Ser	Glu	Val
		50					55					60			Gln
	Gly	Ala	Ala	Trp	Leu	Leu	Ser	Pro	Arg	Leu	Cys	Asp	Val	Met	Leu
	65				70						75				80
20	Thr	Ala	Ser	Ile	Phe	Asn	Leu	Cys	Ala	Ile	Ser	Val	Asp	Arg	Phe
				85						90					95
	Ala	Val	Ala	Val	Pro	Leu	Arg	Tyr	Asn	Arg	Gln	Gly	Gly	Ser	Arg
				100					105					110	Arg
	Gln	Leu	Leu	Leu	Ile	Gly	Ala	Thr	Trp	Leu	Leu	Ser	Ala	Ala	Val
			115				120						125		Ala
25	Ala	Pro	Val	Leu	Cys	Gly	Leu	Asn	Asp	Val	Arg	Gly	Arg	Asp	Pro
			130				135					140			Ala
	Val	Cys	Arg	Leu	Glu	Asp	Arg	Asp	Tyr	Val	Val	Tyr	Ser	Ser	Val
	145					150					155				Cys
30	Ser	Phe	Phe	Leu	Pro	Cys	Pro	Leu	Leu	Tyr	Trp	Ala	Thr	Phe	Arg
				165						170					Gly
	Leu	Gln	Leu	Val	Ala	Arg	Arg	Ala	Lys	Leu	His	Gly	Arg	Ala	Pro
				180					185					190	Arg
	Arg	Pro	Ser	Gly	Pro	Gly	Pro	Pro	Ser	Pro	Thr	Pro	Pro	Ala	Pro
			195					200					205		Arg
35	Leu	Pro	Gln	Asp	Pro	Cys	Gly	Ala	Leu	Pro	Pro	Gln	Thr	Pro	Pro
		210					215					220			Gln
	Thr	Arg	Arg	Arg	Arg	Arg	Ala	Lys	Ile	Thr	Gly	Arg	Glu	Arg	Lys
	225					230					235				240
40	Met	Arg	Val	Leu	Pro	Val	Val	Val	Gly	Ala	Phe	Ile	Leu	Cys	Trp
				245						250					255
	Pro	Phe	Phe	Val	Val	His	Ile	Thr	Gln	Ala	Leu	Cys	Pro	Ala	Cys
				260					265					270	Ser
	Val	Pro	Pro	Arg	Leu	Val	Ser	Ala	Val	Thr	Trp	Leu	Ser	Tyr	Val
				275				280					285		Asn
45	Ser	Ala	Ile	Asn	Pro	Val	Ile	Tyr	Thr	Val	Phe	Asn	Ala	Glu	Phe
		290					295					300			Arg
	Asn	Val	Phe	Arg	Lys	Ala	Leu	Arg	Ala	Cys	Cys				

	305	310	315
(2)	INFORMATION FOR SEQ ID NO:29:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 327 amino acids		
	(B) TYPE: amino acid		
	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: peptide		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:29:		
Lys	Ile	Ser	Leu
1	5	10	15
Leu	Ser	Asn	Ala
20	25	30	35
His	Thr	Pro	Ala
40	45	50	55
Leu	Val	Ser	Ile
60	65	70	75
Thr	Trp	Asn	Phe
80	85	90	95
Ile	Thr	Cys	Cys
100	105	110	115
Asp	Arg	Tyr	Trp
120	125	130	135
Thr	Ala	Gly	His
140	145	150	155
Ile	Cys	Ile	Ser
160	165	170	175
Glu	Met	Ser	Asp
180	185	190	195
Ser	Thr	Cys	Gly
200	205	210	215
Tyr	Gly	Arg	Ile
220	225	230	235
Ser	Leu	Tyr	Gly
240	245	250	255
Ala	Gly	Ser	Ser
260	265	270	275
Asn	His	Val	Lys
280	285	290	295
Ile	Ser	Ala	Ala
300	305	310	315
Leu	Gly	Ala	Phe
320	325	330	335
Val	Leu	Pro	Ile
340	345	350	355
Asp	Phe	Phe	Thr
360	365	370	375
Trp	Leu	Gly	Tyr
380	385	390	395
Ile	Asn	Ser	Ile
400	405	410	415
Leu	Ile	Asn	Pro
420	425	430	435
Pro	Ala	Leu	Phe
440	445	450	455
Thr	Leu	Gly	Ile
460	465	470	475
Arg	Lys	Arg	Val
480	485	490	495
Thr	Gly	Ser	His
500	505	510	515
Ala	Glu	Arg	Glu
520	525	530	535
His	Gly	Glu	His
540	545	550	555
Val	Val	Val	Ser
560	565	570	575
Leu	Ser	Leu	Phe
580	585	590	595
Pro	Ala	Leu	Phe
600	605	610	615
Thr	Gly	Tyr	Ile
620	625	630	635
Asn	Ser	Ile	Asn
640	645	650	655
Pro	Ile	Asn	Pro
660	665	670	675
Ile	Asn	Ser	Ile
680	685	690	695
Val	Leu	Gly	Tyr
700	705	710	715
Thr	Leu	Gly	Tyr
720	725	730	735
Asp	Ser	Cys	Trp
740	745	750	755
Arg	Asp	Ser	Cys
760	765	770	775
Thr	Leu	Gly	Tyr
780	785	790	795
Pro	Ile	Asn	Pro
800	805	810	815
Val	Leu	Gly	Tyr
820	825	830	835
Thr	Leu	Gly	Tyr
840	845	850	855
Asp	Ser	Cys	Trp
860	865	870	875
Arg	Asp	Ser	Cys
880	885	890	895
Thr	Leu	Gly	Tyr
900	905	910	915
Pro	Ile	Asn	Pro
920	925	930	935
Val	Leu	Gly	Tyr
940	945	950	955
Thr	Leu	Gly	Tyr

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Ile Tyr Thr Val Phe Asn Glu Glu Phe Arg Gln Ala Phe Gln Lys Ile
 305 310 315 320

Val Pro Phe Arg Lys Ala Ser
 325

5 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Val Ile Thr Ser Leu Leu Leu Gly Thr Leu Ile Phe Cys Ala Val Leu
 1 5 10 15

Gly Asn Ala Cys Val Val Ala Ala Ile Ala Leu Glu Arg Ser Leu Gln
 20 25 30

Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val Arg Asp Leu Met
 35 40 45

Val Ser Val Leu Val Leu Pro Met Ala Ala Leu Tyr Gln Val Leu Asn
 50 55 60

Lys Trp Thr Leu Gly Gln Val Thr Cys Asp Leu Phe Ile Ala Leu Asp
 65 70 75 80

Val Leu Cys Cys Thr Ser Ser Ile Leu His Leu Cys Ala Ile Ala Leu
 85 90 95

Asp Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asp Tyr Val Asn Lys Arg
 100 105 110

Thr Pro Arg Pro Arg Ala Leu Ile Ser Leu Thr Trp Leu Ile Gly Phe
 115 120 125

Leu Ile Ser Ile Pro Pro Met Leu Gly Trp Arg Thr Pro Glu Asp Arg
 130 135 140

Ser Asp Pro Asp Ala Cys Thr Ile Ser Lys Asp His Gly Tyr Thr Ile
 145 150 155 160

Tyr Ser Thr Ile Phe Ala Phe Tyr Ile Pro Leu Leu Leu Met Leu Val
 165 170 175

Leu Tyr Gly Arg Ile Phe Arg Ala Ala Arg Phe Arg Ile Arg Lys Thr
 180 185 190

Val Lys Lys Val Glu Lys Thr Gly Ala Asp Thr Arg His Gly Ala Ser
 195 200 205

Pro Ala Pro Gln Pro Lys Lys Ser Val Asn Gly Glu Ser Gly Ser Arg
 210 215 220

Asn Ala Ser Phe Glu Arg Lys Asn Glu Arg Asn Ala Phe Ala Lys Leu
 225 230 235 240

Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met Thr
 245 250 255

Phe Ile Leu Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val Leu Pro
 260 265 270

Phe Cys Glu Ser Ser Cys His Met Pro Thr Leu Ile Arg Ala Ile Ile

[illegible]

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Lys Val Leu Gly Ile Val Phe Phe Val Phe Leu Ile Met Trp Cys Pro
 260 265 270
 Phe Phe Ile Thr Asn Ile Leu Ser Val Leu Cys Gly Lys Ala Cys Asn
 275 280 285
 5 Gln Cys Lys Leu Leu Asn Val Phe Val Trp Ile Gly Tyr Val Cys Ser
 290 295 300
 Gly Ile Asn Pro Val Ile Tyr Thr Leu Phe Asn Lys Ile Tyr Arg Arg
 305 310 315 320
 10 Ala Phe Ser Lys Tyr Leu Arg Cys Asp Tyr Lys Pro Asp Lys Lys Pro
 325 330 335
 Pro Val Arg Gln Ile Pro Arg Val Ala Ala Thr Ala Leu Ser Gly Arg
 340 345 350
 Glu Leu Asn Val Asn Ile Tyr Arg His Thr Asn Glu Arg Val Ala Arg
 355 360 365
 15 Lys Ala Asn Asp Pro Glu Pro Gly Ile Glu Asn Gln Val Glu Asn Leu
 370 375 380
 Glu
 385

(2) INFORMATION FOR SEQ ID NO:32:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
 Lys Asn Trp Ser Ala Leu Leu Thr Thr Val Val Ile Ile Leu Thr Ile
 1 5 10 15
 30 Ala Gly Asn Ile Leu Val Ile Met Ala Val Ser Leu Glu Lys Lys Leu
 20 25 30
 Gln Asn Ala Thr Asn Tyr Phe Leu Met Ser Leu Ala Ile Ala Asp Met
 35 40 45
 Leu Leu Gly Phe Leu Val Trp Val Ser Asn Glu Thr Ile Leu Tyr Gly
 50 55 60
 35 Tyr Arg Trp Pro Leu Pro Ser Lys Leu Cys Ala Ile Trp Ile Tyr Leu
 65 70 75 80
 Asp Val Leu Phe Ser Thr Ala Ser Ile Met His Leu Cys Ala Ile Ser
 85 90 95
 40 Leu Asp Arg Tyr Val Ala Ile Gln Asn Pro Ile His His Ser Arg Phe
 100 105 110
 Asn Ser Arg Thr Lys Ala Phe Leu Lys Ile Ile Ala Val Trp Thr Ile
 115 120 125
 Ser Val Gly Ile Ser Met Pro Ile Pro Val Phe Gly Leu Gln Asp Asp
 130 135 140
 45 Ser Lys Val Phe Lys Glu Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe
 145 150 155 160

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Val Leu Ile Gly Ser Phe Val Ala Phe Phe Ile Pro Leu Thr Ile Met
165 170 175

Val Ile Thr Tyr Phe Leu Thr Ile Lys Ser Leu Arg Gln Lys Phe Ala
180 185 190

5 Thr Leu Cys Val Ser Asp Leu Ser Thr Arg Ala Lys Leu Ala Ser Phe
195 200 205

Ser Phe Leu Pro Gln Ser Ser Leu Ser Ser Glu Lys Leu Phe Gln Arg
210 215 220

10 Ser Ile His Arg Glu Pro Gly Ser Tyr Ala Gly Arg Lys Thr Met Gln
225 230 235 240

Ser Ile Ser Asn Glu Gln Lys Ala Cys Lys Val Leu Gly Ile Val Phe
245 250 255

Phe Leu Phe Val Val Met Trp Cys Pro Phe Phe Ile Thr Asn Ile Met
260 265 270

15 Val Ile Cys Lys Glu Ser Cys Asn Glu Asn Val Ile Gly Ala Leu Leu
275 280 285

Asn Val Phe Val Trp Ile Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu
290 295 300

20 Val Tyr Thr Leu Phe Asn Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr
305 310 315 320

Leu Gln Cys Gln Tyr Lys Glu Asn Arg Lys Pro Leu Leu Ile Leu Val
325 330 335

Asn Thr Ile Pro Ala Leu Ala Tyr Lys Ser Ser Gln Leu Gln Val Gly
340 345 350

25 Gln Lys Lys Asn Ser Gln Glu Asp Ala Glu Gln Thr Val Asp Asp Cys
355 360 365

Ser Met Val Thr Leu Gly Lys Gln Gln Ser Glu
370 375

(2) INFORMATION FOR SEQ ID NO:33:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Thr Ile Thr Val Val Leu Ala Val Leu Ile Leu Ile Thr Val Ala
1 5 10 15

Gly Asn Val Val Val Cys Ile Ala Val Gly Ile Asn Arg Arg Leu Arg
20 25 30

Asn Leu Thr Asn Cys Phe Ile Val Ser Leu Ala Ile Thr Asp Leu Leu
35 40 45

Leu Gly Leu Leu Val Leu Pro Phe Ser Ala Ile Tyr Gln Leu Ser Cys
50 55 60

45 Lys Trp Ser Phe Gly Lys Val Phe Cys Asn Ile Tyr Thr Ser Leu Asp
65 70 75 80

Val Met Leu Cys Thr Ala Ser Ile Leu Asn Leu Leu Ile Ser Leu Asp

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	85	90	95
	Arg Tyr Cys Ala Val Met Asp Pro Leu Arg Tyr Pro Val Leu Val Arg		
	100	105	110
5	Pro Val Arg Val Ala Ile Ser Leu Val Leu Ile Trp Val Ile Ser Ile		
	115	120	125
	Thr Leu Ser Phe Leu Ser Ile His Leu Gly Trp Asn Ser Arg Asn Glu		
	130	135	140
	Thr Ser Lys Gly Asn His Thr Thr Ser Lys Cys Lys Val Gln Val Asn		
	145	150	155
10	Glu Val Tyr Gly Leu Val Asp Gly Leu Val Thr Phe Tyr Leu Pro Leu		
	165	170	175
	Leu Ile Met Cys Ile Thr Tyr Tyr Arg Ile Phe Lys Val Ala Arg Asp		
	180	185	190
15	Ala Lys Arg Asn His Ile Ser Ser Trp Lys Ala Ala Thr Ile Arg Glu		
	195	200	205
	His Lys Ala Thr Val Thr Ile Ala Ala Val Met Ala Phe Ile Ile Cys		
	210	215	220
	Trp Phe Pro Tyr Phe Thr Ala Phe Val Tyr Arg Gly Leu Arg Gly Asp		
	225	230	235
20	Asp Ala Ile Asn Glu Val Leu Glu Ala Ile Val Leu Trp Leu Gly Tyr		
	245	250	255
	Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr Ala Ala Leu Asn Arg Asp		
	260	265	270
25	Phe Arg Thr Gly Tyr Gln Gln Leu Phe Cys Cys Arg Ile Ala Asn Arg		
	275	280	285
	Asn Ser His Lys Thr Ser Leu Arg Ser Asn Ala Ser Gln Leu Ser Arg		
	290	295	300
	Thr Gln Ser Arg Glu Pro Arg Gln Gln Glu Glu Lys Pro Leu Lys Leu		
	305	310	315
30	Gln Val Trp Ser Gly Thr Glu Val Thr Ala Pro Gln Gly Ala Thr Asp		
	325	330	335
	Arg		

(2) INFORMATION FOR SEQ ID NO:34:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ile	Ile	Thr	Tyr	Leu	Val	Phe	Ala	Val	Arg	Phe	Val	Leu	Gly	Val	Leu
1				5					10					15	

Gly	Asn	Gly	Leu	Val	Ile	Trp	Val	Ala	Gly	Phe	Arg	Met	Thr	His	Thr
			20					25					30		

Val	Thr	Thr	Ile	Ser	Tyr	Leu	Asn	Leu	Ala	Val	Ala	Asp	Phe	Cys	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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	35	40	45
	Thr Ser Thr Leu Pro Phe	Phe Met Val Arg Leu Gly	His Trp Pro Phe
	50	55	60
5	Gly Trp Phe Leu Cys Lys	Phe Leu Phe Thr Ile Val	Asp Ile Asn Leu
	65	70	75 80
	Phe Gly Ser Val Phe Leu Ile	Ala Leu Ile Ala Leu Asp	Arg Cys Val
		85	90 95
	Cys Val Leu His Pro Val Trp	Thr Gln Asn His Arg Thr	Val Ser Leu
		100	105 110
10	Ala Lys Lys Val Ile Ile Gly	Pro Trp Val Met Ala Leu	Leu Leu Thr
		115	120 125
	Leu Pro Val Ile Ile Arg Val	Thr Ile Val Pro Gly Lys	Thr Gly Thr
		130	135 140
15	Val Ala Cys Thr Phe Asn Phe	Ser Pro Trp Thr Asn Asp	Pro Lys Glu
		145	150 155 160
	Arg Ile Asn Val Ala Val Ala	Met Leu Thr Val Arg Gly	Ile Ile Arg
		165	170 175
	Phe Ile Ile Gly Phe Ser Ala	Pro Met Ser Ile Val Ala	Val Ser Tyr
		180	185 190
20	Gly Leu Ile Ala Thr Lys Ile	Ile Lys Ser Ser Arg Pro	Leu Arg Val
		195	200 205
	Leu Ser Phe Val Ala Ala Ala	Phe Phe Leu Cys Trp Ser	Pro Tyr Gln
		210	215 220
25	Val Val Ala Leu Ile Ala Thr	Val Arg Ile Arg Glu Leu	Leu Gln Gly
		225	230 235 240
	Met Tyr Lys Glu Ile Gly Ile	Ala Val Asp Val Thr Ser	Ala Ile Ala
		245	250 255
	Phe Phe Asn Ser Cys Leu Asn	Pro Leu Tyr Val Phe Met	Gly Gln Asp
		260	265 270
30	Phe Arg Glu Arg Leu Ile His	Ala Leu Pro Ala Ser Leu	Glu Arg Ala
		275	280 285
	Leu Thr Glu Asp Ser Thr Gln	Thr Ser Asp Thr Ala Thr	Asn Ser Thr
		290	295 300
35	Leu Pro Ser Ala Glu Val Ala	Leu Gln Ala Lys	
		305	310 315

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 304 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

45 Asp Ile Leu Ala Leu Val Ile Phe Ala Val Val Phe Leu Val Gly Val
 1 5 10 15

Leu Gly Asn Ala Leu Val Val Trp Val Thr Ala Phe Glu Ala Lys Arg

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	20	25	30
	Thr Ile Asn Ala Ile Trp Phe Leu Asn Ile Ala Val Ala Asp Phe Leu 35 40 45		
5	Ser Cys Leu Ala Leu Pro Ile Leu Phe Thr Ser Ile Val Gln His His 50 55 60		
	His Trp Pro Phe Gly Gly Ala Ala Cys Ser Ile Leu Pro Ser Leu Ile 65 70 75 80		
	Leu Leu Asn Met Tyr Ala Ser Ile Leu Leu Leu Ala Thr Ile Ser Ala 85 90 95		
10	Asp Arg Phe Leu Leu Val Phe Lys Pro Ile Trp Cys Gln Asn Phe Arg 100 105 110		
	Gly Ala Gly Leu Ala Trp Ile Ala Cys Ala Val Ala Trp Gly Ile Ala 115 120 125		
15	Leu Leu Leu Thr Ile Pro Ser Phe Leu Tyr Arg Val Val Arg Glu Glu 130 135 140		
	Tyr Phe Pro Pro Lys Val Leu Cys Gly Cys Asp Tyr Ser His Asp Lys 145 150 155 160		
	Arg Arg Glu Arg Ala Val Ala Ile Val Arg Leu Val Leu Gly Phe Leu 165 170 175		
20	Trp Pro Leu Leu Thr Leu Thr Ile Cys Tyr Thr Thr Arg Ser Thr Lys 180 185 190		
	Thr Leu Lys Val Val Val Ala Val Val Ala Ser Phe Phe Ile Phe Trp 195 200 205		
25	Leu Pro Tyr Gln Val Thr Gly Ile Met Met Ser Phe Leu Glu Pro Ser 210 215 220		
	Ser Pro Thr Phe Leu Leu Leu Asn Lys Leu Asp Ser Leu Cys Val Ser 225 230 235 240		
	Phe Ala Tyr Ile Asn Cys Cys Ile Asn Pro Ile Ile Tyr Val Val Ala 245 250 255		
30	Gly Gln Gly Gln Phe Gln Gly Arg Leu Arg Lys Ser Leu Pro Ser Leu 260 265 270		
	Leu Arg Asn Val Leu Thr Glu Glu Ser Val Val Arg Glu Ser Lys Ser 275 280 285		
35	Phe Thr Arg Ser Thr Val Asp Thr Met Ala Gln Lys Thr Gln Ala Val 290 295 300		

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

45 Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val Phe Val Val Ser Leu
1 5 10 15

Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile Leu Lys Met Lys Val

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	20	25	30
	Lys Lys Pro Ala Val His Ile Ala Thr Ala Asp Val Leu Phe Val Ser		
	35	40	45
5	Val Leu Pro Phe Lys Ile Ser Tyr Tyr Phe Ser Gly Ser Asp Trp Gln		
	50	55	60
	Phe Gly Ser Glu Leu Cys Arg Phe Val Thr Ala Ala Phe Tyr Cys Asn		
	65	70	75
	Met Tyr Ala Ser Ile Leu Leu Ile Ser Ile Asp Arg Phe Ile Ala Val		
	85	90	95
10	Val Tyr Pro Met Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser		
	100	105	110
	Phe Thr Cys Ile Ala Ile Trp Ala Ile Ala Ile Ala Gly Val Pro Leu		
	115	120	125
15	Val Leu Lys Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr		
	130	135	140
	Ile Cys His Asp Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala		
	145	150	155
	Tyr Tyr Phe Ser Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu Ile		
	165	170	175
20	Ile Ser Thr Val Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser		
	180	185	190
	Ala Val Ala Asn Arg Ser Lys Lys Ser Arg Thr Asn Arg Cys Phe Asn		
	195	200	205
25	Ser Thr Val Ala Leu Phe Leu Ser Ala Ala Val Phe Cys Ile Phe Ile		
	210	215	220
	Ile Cys Phe Gly Pro Thr Trp Leu Leu Ile Ala His Tyr Ser Phe Leu		
	225	230	235
	Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala Tyr Leu Leu Cys		
	245	250	255
30	Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro Leu Ile Tyr Tyr		
	260	265	270
	Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser Ile Leu Cys Cys		
	275	280	285
35	Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser Gly Gln Leu Met		
	290	295	300
	Ser Leu Thr Cys Ser Ser Asn Leu Asn Asn Ser Ile Tyr Lys Lys Leu		
	305	310	315
	Leu Thr		320

- 40 (2) INFORMATION FOR SEQ ID NO:37:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - 45 (ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

	Tyr	Ile	Asn	Thr	Val	Ile	Ser	Cys	Thr	Ile	Phe	Ile	Val	Gly	Trp	Gly	
	1				5					10					15		
5	Asn	Ala	Thr	Leu	Leu	Arg	Ile	Ile	Tyr	Gln	Asn	Lys	Cys	Met	Arg	Asn	
				20					25					30			
	Gly	Pro	Asn	Ala	Leu	Ile	Ala	Ser	Ile	Ala	Leu	Gly	Asp	Leu	Ile	Tyr	
			35				40						45				
	Val	Val	Ile	Asp	Leu	Pro	Ile	Asn	Val	Pro	Lys	Leu	Ile	Ala	Gly	Arg	
		50					55					60					
10	Trp	Pro	Phe	Glu	Gln	Asn	Asp	Phe	Gly	Val	Phe	Cys	Lys	Phe	Met	Gly	
	65				70						75					80	
	Val	Val	Met	Ile	Phe	Phe	Gly	Leu	Ser	Pro	Leu	Leu	Leu	Gly	Ala	Ala	
				85					90						95		
15	Met	Ala	Ser	Glu	Arg	Tyr	Leu	Gly	Ile	Thr	Arg	Pro	Phe	Ser	Arg	Pro	
				100				105						110			
	Ala	Val	Ala	Ser	Gln	Arg	Arg	Ala	Trp	Ala	Thr	Val	Gly	Leu	Val	Trp	
			115					120					125				
	Ala	Ala	Ala	Leu	Ala	Leu	Gly	Leu	Leu	Pro	Leu	Leu	Gly	Val	Gly	Arg	
		130					135					140					
20	Tyr	Thr	Val	Gln	Tyr	Pro	Gly	Ser	Trp	Cys	Phe	Leu	Thr	Leu	Gly	Ala	
	145				150						155					160	
	Glu	Ser	Gly	Asp	Val	Ala	Phe	Gly	Leu	Leu	Phe	Ser	Gly	Leu	Ser	Val	
				165					170						175		
25	Gly	Leu	Ser	Phe	Leu	Leu	Asn	Thr	Val	Ser	Val	Ala	Thr	Leu	His	His	
				180				185						190			
	Val	Tyr	His	Gly	Gln	Glu	Ala	Ala	Gln	Gln	Arg	Pro	Arg	Asp	Ser	Glu	
			195				200						205				
	Val	Glu	Met	Met	Ala	Gln	Leu	Leu	Gly	Ile	Met	Val	Val	Ala	Ser	Val	
		210					215					220					
30	Cys	Trp	Leu	Pro	Leu	Leu	Val	Phe	Ile	Ala	Gln	Thr	Val	Leu	Arg	Asn	
	225				230						235					240	
	Pro	Pro	Ala	Met	Ser	Pro	Ala	Gly	Gln	Leu	Ser	Arg	Thr	Thr	Glu	Lys	
				245					250						255		
35	Glu	Leu	Leu	Ile	Tyr	Leu	Arg	Val	Ala	Thr	Trp	Asn	Gln	Ile	Leu	Asp	
			260					265						270			
	Pro	Trp	Val	Tyr	Ile	Leu	Phe	Arg	Arg	Ala	Val	Leu	Arg	Arg	Leu	Gln	
			275				280						285				
	Pro	Arg	Leu	Ser	Thr	Arg	Pro	Arg	Ser	Leu	Ser	Leu	Gln	Pro	Gln	Leu	
		290					295					300					
40	Thr	Gln	Arg	Ser	Gly	Leu	Gln										
		305				310											

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	Lys	Tyr	Phe	Val	Val	Ile	Ile	Tyr	Ala	Leu	Val	Phe	Leu	Leu	Ser	Leu	
	1				5					10					15		
5	Leu	Gly	Asn	Ser	Leu	Val	Met	Leu	Val	Ile	Leu	Tyr	Ser	Arg	Gly	Val	
				20					25					30			
	Arg	Ser	Val	Thr	Ile	Val	Tyr	Leu	Leu	Asn	Ile	Ala	Ile	Ala	Asp	Leu	
			35					40					45				
10	Leu	Phe	Ala	Leu	Thr	Leu	Pro	Ile	Trp	Ala	Ala	Ser	Lys	Val	Asn	Gly	
	50						55					60					
	Trp	Ile	Phe	Gly	Thr	Phe	Leu	Cys	Lys	Trp	Ser	Leu	Leu	Lys	Glu	Val	
	65					70					75				80		
	Asn	Phe	Tyr	Ser	Gly	Ile	Leu	Leu	Leu	Ala	Cys	Ile	Ser	Val	Asp	Arg	
					85					90					95		
15	Tyr	Leu	Ala	Ile	Val	Arg	Ala	Thr	Arg	Thr	Leu	Thr	Gln	Lys	Arg	His	
				100					105					110			
	Leu	Val	Lys	Phe	Ile	Cys	Leu	Ser	Ile	Trp	Gly	Leu	Ser	Leu	Leu	Leu	
			115					120					125				
20	Ala	Leu	Pro	Val	Leu	Leu	Phe	Arg	Arg	Thr	Val	Tyr	Ser	Ser	Asn	Val	
			130					135					140				
	Ser	Pro	Ala	Cys	Tyr	Glu	Asp	Met	Gly	Asn	Asn	Tyr	Ala	Asn	Trp	Arg	
	145					150					155					160	
	Met	Leu	Leu	Pro	Ile	Leu	Pro	Gln	Ser	Phe	Gly	Phe	Ile	Val	Pro	Leu	
					165					170					175		
25	Leu	Ile	Met	Leu	Tyr	Cys	Tyr	Gly	Phe	Thr	Leu	Arg	Thr	Leu	Phe	Lys	
				180					185					190			
	Ala	Ile	Met	Gly	Gln	Lys	His	Arg	Ala	Met	Arg	Val	Ile	Phe	Ala	Val	
			195					200					205				
30	Val	Leu	Ile	Phe	Leu	Leu	Cys	Trp	Leu	Pro	Tyr	Asn	Leu	Val	Leu	Ile	
		210					215					220					
	Ala	Asp	Thr	Leu	Met	Arg	Thr	Gln	Val	Ile	Gln	Glu	Thr	Cys	Glu	Arg	
	225					230					235				240		
	Arg	Asn	His	Ile	Asp	Arg	Ala	Ile	Asp	Ala	Thr	Glu	Ile	Leu	Gly	Ile	
					245					250					255		
35	Leu	His	Ser	Cys	Leu	Asn	Pro	Leu	Ile	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	
				260					265					270			
	Phe	Arg	His	Gly	Leu	Leu	Lys	Ile	Leu	Ala	Ile	His	Gly	Leu	Ile	Ser	
			275					280					285				
40	Lys	Asp	Ser	Leu	Pro	Lys	Asp	Ser	Arg	Pro	Ser	Phe	Val	Gly	Ser	Ser	
		290					295						300				
	Ser	Gly	His	Thr	Ser	Thr	Thr	Leu									
		305					310										

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 326 amino acids
(B) TYPE: amino acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

5	Leu Phe Pro Ile Val Tyr Ser Ile Ile Phe Val Leu Gly Ile Ile Ala	1 5 10 15
	Asn Gly Tyr Val Leu Trp Val Phe Ala Arg Leu Tyr Pro Ser Lys Lys	20 25 30
10	Asn Glu Ile Lys Ile Phe Met Val Asn Leu Thr Val Ala Asp Leu Leu	35 40 45
	Phe Leu Ile Thr Leu Pro Leu Trp Ile Val Tyr Tyr Ser Asn Gln Gly	50 55 60
	Asn Trp Phe Leu Pro Lys Phe Leu Cys Asn Leu Ala Gly Cys Leu Phe	65 70 75 80
15	Phe Ile Asn Thr Tyr Cys Ser Val Ala Phe Leu Gly Val Ile Thr Tyr	85 90 95
	Asn Arg Phe Gln Ala Val Lys Tyr Pro Ile Lys Thr Ala Gln Ala Thr	100 105 110
20	Thr Arg Lys Arg Gly Ile Ala Leu Ser Leu Val Ile Trp Val Ala Ile	115 120 125
	Val Ala Ala Ala Ser Tyr Phe Leu Val Met Met Asp Ser Thr Asn Val	130 135 140
	Val Ser Asn Lys Ala Gly Ser Gly Asn Ile Thr Arg Cys Phe Glu Arg	145 150 155 160
25	Tyr Glu Lys Gly Ser Lys Pro Val Leu Ile Ile His Ile Cys Ile Val	165 170 175
	Leu Gly Phe Phe Ile Val Phe Leu Leu Ile Leu Phe Cys Asn Leu Val	180 185 190
30	Ile Ile His Thr Leu Leu Arg Gly Pro Val Lys Gln Gln Arg Asn Ala	195 200 205
	Glu Val Arg Arg Arg Ala Leu Trp Met Val Cys Thr Val Ile Ala Val	210 215 220
	Phe Val Ile Cys Phe Val Pro His His Met Val Gln Leu Pro Trp Thr	225 230 235 240
35	Leu Ala Glu Leu Gly Met Trp Pro Ser Ser Asn His Gln Ala Ile Asn	245 250 255
	Asp Ala His Gln Val Thr Leu Cys Leu Leu Ser Thr Asn Cys Val Leu	260 265 270
40	Asp Pro Val Ile Tyr Cys Phe Leu Thr Lys Lys Phe Arg Lys His Leu	275 280 285
	Ser Glu Lys Leu Asn Ile Met Arg Ser Ser Gln Lys Cys Ser Arg Val	290 295 300
	Thr Arg Asp Thr Gly Thr Glu Met Ala Ile Pro Ile Asn His Thr Pro	305 310 315 320
45	Val Asn Pro Ile Lys Asn	

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(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

10 Tyr Ile Asn Thr Ile Val Ser Cys Leu Val Phe Val Leu Gly Ile Ile
 1 5 10 15

Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lys Asn Lys Cys Met Arg
 20 25 30

15 Asn Gly Pro Asn Ile Leu Ile Ala Ser Ile Ala Leu Gly Asp Leu Leu
 35 40 45

His Ile Ile Ile Asp Ile Pro Ile Met Ala Tyr Lys Leu Ile Ala Gly
 50 55 60

Asp Trp Pro Phe Ala Cys Lys Leu Phe Pro Phe Leu Gln Lys Ser Ser
 65 70 75 80

20 Val Gly Ile Thr Val Leu Asn Leu Cys Ala Leu Ser Val Asp Arg Tyr
 85 90 95

Arg Ala Val Ala Ser Trp Ser Arg Val Gln Gly Ile Gly Ile Pro Leu
 100 105 110

25 Val Thr Ala Ile Glu Ile Val Ser Ile Trp Ile Leu Ser Phe Ile Leu
 115 120 125

Ala Ile Pro Glu Ala Ile Gly Phe Trp Met Val Pro Phe Glu Tyr Lys
 130 135 140

Gly Ala Gln His Arg Thr Cys Met Leu Asn Ala Thr Ser Lys Leu Phe
 145 150 155 160

30 Tyr Gln Asp Val Lys Asp Trp Trp Leu Phe Gly Phe Tyr Phe Leu Leu
 165 170 175

Val Cys Thr Ala Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn
 180 185 190

35 Arg Arg Asn Gly Ser Leu Arg Ile Ala Leu Ser Glu His Leu Lys Gln
 195 200 205

Arg Arg Glu Val Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala
 210 215 220

Leu Cys Trp Phe Pro Leu His Leu Ser Arg Ile Leu Lys Lys Thr Val
 225 230 235 240

40 Tyr Asp Glu Met Asp Thr Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu
 245 250 255

Leu Met Tyr Ile Gly Ile Asn Thr Ala Thr Met Ser Cys Ile Asn Pro
 260 265 270

45 Ile Ala Leu Tyr Phe Val Ser Lys Lys Phe Lys Asn Cys Phe Gln Ser
 275 280 285

Cys Leu Cys Cys Cys Cys Tyr Gln Ser Lys Ser Ile Met Thr Ser Val
 290 295 300

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Pro Met Gln Gly Thr Ser Ile Gln Trp Lys Asn His Glu Gln Asn Asn
 305 310 315 320

His Asn Thr Glu Arg Ser Ser His Lys Asp Ser Ile Asn
 325 330

5 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Ile Ala Ser Pro Trp Phe Ala Ala Ser Phe Cys Val Val Gly Leu
 1 5 10 15

Ala Ser Asn Leu Leu Ala Leu Ser Val Leu Ala Gly Ala Arg Gln Ser
 20 25 30

Ser Ser His Thr Arg Ser Ser Phe Leu Thr Phe Leu Cys Gly Leu Val
 35 40 45

Leu Thr Leu Asp Phe Leu Gly Leu Leu Val Thr Gly Thr Ile Val Val
 50 55 60

Ser Gln His Ala Ala Leu Phe Glu Trp His Ala Val Asp Pro Gly Cys
 65 70 75 80

Arg Leu Cys Arg Leu Val Pro Phe Ile Gln Lys Ala Ser Val Gly Ile
 85 90 95

Thr Val Leu Ser Leu Cys Ala Leu Ser Ile Asp Arg Tyr Arg Ala Val
 100 105 110

Ala Ser Trp Ser Arg Ile Lys Gly Ile Gly Val Pro Lys Trp Thr Ala
 115 120 125

Val Glu Ile Val Leu Ile Trp Val Val Ser Val Val Leu Ala Val Pro
 130 135 140

Glu Ala Ile Gly Phe Asp Thr Thr Ser Asp Tyr Lys Gly Lys Pro Leu
 145 150 155 160

Arg Val Cys Met Leu Asn Pro Phe Gln Lys Thr Ala Phe Met Phe Tyr
 165 170 175

Lys Thr Ala Ala Lys Asp Trp Trp Leu Phe Ala Phe Tyr Phe Cys Leu
 180 185 190

Pro Leu Ala Ile Thr Ala Ile Phe Tyr Thr Leu Met Thr Cys Glu Met
 195 200 205

Leu Arg Lys Lys Ser Gly Met Gln Ile Ala Leu Asn Asp His Leu Lys
 210 215 220

Gln Arg Arg Glu Val Ala Lys Thr Val Phe Cys Leu Val Leu Val Phe
 225 230 235 240

Ala Leu Cys Trp Leu Pro Leu His Leu Ser Arg Ile Leu Lys Leu Thr
 245 250 255

Leu Tyr Asp Gln Ser Asn Pro Gln Arg Cys Glu Leu Leu Ser Phe Leu
 260 265 270

Leu Val Leu Asp Tyr Ile Gly Ile Asn Met Ala Ser Ile Asn Ser Cys

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275 280 285

Ile Asn Pro Ile Ala Leu Tyr Leu Val Ser Lys Arg Phe Lys Asn Cys
 290 295 300

5 Phe Lys Ser Cys Leu Cys Cys Trp Cys Gln Thr Phe Glu Glu Lys Gln
 305 310 315 320

Ser Leu Glu Glu Lys Gln Ser Cys Leu Lys Phe Lys Ala Asn Asp His
 325 330 335

Gly Tyr Asp Asn Phe Arg Ser Ser Asn Lys Tyr Ser Ser Ser
 340 345 350

10 (2) INFORMATION FOR SEQ ID NO:42:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
 Ile Tyr Val Ile Pro Ala Val Tyr Gly Leu Ile Ile Val Ile Gly Leu
 1 5 10 15
 20 Ile Gly Asn Ile Thr Leu Ile Lys Ile Phe Cys Thr Val Lys Ser Leu
 20 25 30

Asn Leu Phe Ile Ser Ser Ile Ala Leu Gly Asp Leu Leu Leu Val
 35 40 45

25 Thr Ile Cys Ala Pro Val Asp Ala Ser Lys Tyr Ile Ala Asp Arg Trp
 50 55 60

Leu Phe Gly Arg Ile Gly Cys Lys Leu Ile Pro Phe Ile Gln Leu Thr
 65 70 75 80

Ser Val Gly Val Ser Val Phe Thr Leu Thr Ala Leu Ser Ala Asp Arg
 85 90 95

30 Tyr Lys Ala Ile Val Arg Pro Thr Cys Ile Gln Ala Ser Leu Ile Cys
 100 105 110

Leu Lys Ala Ala Leu Ile Trp Ile Val Ser Leu Leu Ala Ile Pro Glu
 115 120 125

35 Ala Val Phe Ser Asp Leu His Pro Phe His Val Lys Asp Thr Asn Gln
 130 135 140

Thr Phe Ile Ser Cys Ala Pro Tyr Pro His Ser Asn Glu Leu His Pro
 145 150 155 160

Lys Ile His Ser Met Ala Ser Phe Leu Val Phe Tyr Val Ile Pro Leu
 165 170 175

40 Ala Ile Ile Ser Val Tyr Tyr Tyr Phe Ile Ala Arg Asn Leu Ile Gln
 180 185 190

Ser Ala Tyr Asn Leu Pro Val Glu Gly Asn Ile His Val Lys Lys Gln
 195 200 205

45 Ile Glu Ser Arg Lys Arg Leu Ala Lys Thr Val Leu Val Phe Val Gly
 210 215 220

Leu Phe Ala Phe Cys Trp Leu Pro Asn His Val Ile Tyr Leu Tyr Arg
 225 230 235 240

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Ser Tyr His Tyr Ser Glu Val Asp Thr Ser Met Leu His Phe Val Thr
 245 250 255
 Ser Ile Cys Ala Arg Leu Leu Ala Pro Thr Asn Ser Cys Val Asn Pro
 260 265 270
 5 Phe Ala Leu Tyr Leu Leu Ser Lys Ser Phe Arg Gln Phe Asn Thr Gln
 275 280 285
 Leu Leu Cys Cys Gln Pro Gly Leu Ser His Ser Thr Gly Arg Ser Leu
 290 295 300
 10 Ser Phe Lys Ser Thr Asn Pro Ser Ala Thr Phe Ser Leu Ile Asn Arg
 305 310 315 320
 Asn Ile Cys His Glu Gly Tyr Val
 325
 (2) INFORMATION FOR SEQ ID NO:43:
 (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 345 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
 Cys Val Ile Pro Ser Ser Leu Tyr Leu Ile Ile Ile Ser Val Gly Leu
 1 5 10 15
 Leu Gly Asn Ile Met Leu Val Lys Ile Phe Leu Thr Asn Ser Thr Met
 20 25 30
 25 Arg Ser Val Pro Asn Ile Phe Ile Ser Asn Ile Ala Ala Gly Asp Leu
 35 40 45
 Leu Leu Leu Leu Thr Cys Val Pro Val Asp Ala Ser Arg Tyr Phe Phe
 50 55 60
 30 Asp Glu Trp Val Phe Gly Lys Leu Ile Gly Cys Lys Leu Ile Pro Ala
 65 70 75 80
 Ile Gln Leu Thr Ser Val Gly Val Ser Val Pro Thr Leu Thr Ala Leu
 85 90 95
 Ser Ala Asp Arg Tyr Arg Ala Ile Val Asn Pro Met Asp Met Thr Ser
 100 105 110
 35 Gly Val Val Leu Trp Thr Ser Val Ala Val Gly Ile Trp Val Val Ser
 115 120 125
 Val Leu Leu Ala Val Pro Glu Ala Val Phe Ser Glu Val Ala Arg Ile
 130 135 140
 40 Gly Ser Ser Asp Asn Ser Ser Phe Thr Ala Cys Ile Pro Tyr Pro Gln
 145 150 155 160
 Thr Asp Glu Leu His Pro Lys Ile His Ser Val Leu Ile Phe Leu Val
 165 170 175
 Tyr Phe Leu Ile Pro Leu Val Ile Ile Ser Ile Tyr Tyr Tyr His Ile
 180 185 190
 45 Ala Lys Thr Leu Ile Arg Ser Ala His Asn Leu Pro Gly Glu Tyr Asn
 195 200 205
 Glu His Thr Lys Lys Gln Met Glu Thr Arg Lys Arg Leu Ala Lys Ile

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	210		215		220
	Val Leu Val Phe Val Gly Cys Phe Val Phe Cys Trp Phe Pro Asn His				
	225		230		235
5	Ile Leu Tyr Leu Tyr Arg Ser Phe Asn Tyr Lys Glu Ile Asp Pro Ser				
		245		250	255
	Leu Gly Thr Cys Val Thr Leu Val Ala Arg Val Leu Ser Phe Ser Asn				
		260		265	270
	Ser Cys Val Asn Pro Phe Ala Leu Tyr Leu Leu Ser Glu Ser Phe Arg				
		275		280	285
10	Lys His Phe Ser Asn Gln Leu Cys Cys Gly Gln Lys Ser Tyr Pro Glu				
		290		295	300
	Arg Ser Thr Ser Tyr Leu Leu Ser Ser Ser Ala Val Trp Arg Ser Leu				
		305		310	315
15	Lys Ser Asn Ala Lys Asn Val Val Thr Asn Ser Val Leu Ile Asn Gly				
		325		330	335
	His Ser Thr Lys Gln Glu Ile Ala Leu				
		340		345	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

20	Tyr Thr Leu Ser Phe Ile Tyr Ile Phe Ile Phe Val Ile Cys Glx Leu
	1 5 10 15
	Leu Ala Asn Ser Val Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr
	20 25 30
30	Gly Tyr Asp Thr His Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu
	35 40 45
	Trp Trp Leu Thr Ile Pro Val Trp Trp Ser Leu Val Gln His Asn Gln
	50 55 60
35	Trp Pro Met Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser
	65 70 75 80
	Ile Asn Leu Phe Ser Gly Ile Phe Phe Leu Thr Cys Met Ser Val Asp
	85 90 95
	Arg Tyr Leu Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys
	100 105 110
40	Lys Met Val Arg Arg Ala Val Cys Ile Leu Val Trp Leu Leu Ala Phe
	115 120 125
	Cys Val Ser Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala
	130 135 140
45	Ser Asn Asn Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile
	145 150 155 160
	Lys Glu Trp Leu Ile Ser Leu Leu Val Ser Val Val Leu Ile Gly Phe
	165 170 175

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Ala Val Pro Phe Ser Ile Ile Ala Val Phe Tyr Phe Ser Leu Ile Ala
180 185 190

Arg Ala Ile Ser Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys
195 200 205

5 Ile Ile Phe Ser Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr
210 215 220

His Val Ala Val Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro
225 230 235 240

10 Phe Thr Cys Arg Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr
245 250 255

Gln Cys Leu Ser Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser
260 265 270

Phe Ile Asn Arg Asn Tyr Arg Tyr Glu Ile Asn Trp Ile Phe Lys Tyr
275 280 285

15 Ser Ala Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser
290 295 300

Glx Thr Glu Tyr Ser Ala Leu Glu Gln Asn Ala Lys
305 310 315

(2) INFORMATION FOR SEQ ID NO:45:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Lys Val Leu Val Thr Ala Ile Tyr Leu Ala Leu Phe Val Val Gly Thr
1 5 10 15

30 Val Gly Asn Ser Val Thr Ala Phe Thr Leu Ala Arg Lys Lys Ser Leu
20 25 30

Gln Ser Leu Gln Ser Thr Val His Tyr His Leu Ser Ser Leu Ala Leu
35 40 45

Ser Asp Leu Leu Ile Leu Leu Trp Val Glu Leu Tyr Asn Phe Ile Trp
50 55 60

35 His His Pro Trp Ala Phe Gly Asp Ala Gly Cys Arg Gly Tyr Tyr Phe
65 70 75 80

Leu Arg Asp Ala Cys Thr Tyr Ala Thr Ala Leu Asn Val Ala Ser Leu
85 90 95

40 Ser Val Glu Arg Tyr Leu Ala Ile Cys His Pro Phe Lys Ala Lys Thr
100 105 110

Leu Met Ser Arg Ser Arg Thr Lys Lys Phe Ile Ser Ala Ile Trp Leu
115 120 125

Ala Ser Ala Leu Leu Ala Ile Pro Met Leu Phe Thr Leu Gly Leu Gln
130 135 140

45 Asn Arg Ser Gly Asp Gly Thr His Pro Gly Gly Leu Val Cys Thr Pro
145 150 155 160

Ile Val Asp Thr Ala Thr Val Lys Val Val Ile Gln Val Asn Thr Phe

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	165	170	175
	Met Ser Phe Leu Phe Pro Met Leu Val Ile Ser Ile Leu Asn Thr Val		
	180	185	190
5	Ile Ala Asn Lys Leu Thr Val Met Val His Gln Ala Ala Glu Gln Gly		
	195	200	205
	Arg Val Cys Thr Val Gly Thr His Asn Gly Leu Glu His Ser Thr Phe		
	210	215	220
	Asn Met Arg Ile Glu Pro Gly Arg Val Gln Ala Leu Arg His Gly Val		
	225	230	235
10	Leu Val Leu Arg Ala Val Val Ile Ala Phe Val Val Cys Trp Leu Pro		
	245	250	255
	Tyr Leu Cys Tyr Ile Ser Asp Glu Gln Trp Arg Thr Phe Leu Phe Asp		
	260	265	270
15	Phe Tyr His Tyr Phe Tyr Met Leu Thr Asn Ala Leu Phe Tyr Val Ser		
	275	280	285
	Ser Ala Ile Asn Pro Ile Leu Tyr Asn Leu Val Ser Ala Asn Phe Arg		
	290	295	300
	Gln Val Phe Leu Ser Thr Leu Ala Cys Leu Phe Cys Pro Gly Trp Pro		
	305	310	315
20	Leu Ile Arg Arg Lys Lys Arg Pro Thr Phe Ser Arg Lys Pro Asn Ser		
	325	330	335
	Met Ser Ser Asn His Ala Phe Ser Thr Ser Ala Thr Arg Phe Thr Leu		
	340	345	350
25	Tyr		

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

35	Ala Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Leu Leu Ala Ala Leu	
	1	15
	Glu Asn Ile Phe Val Leu Ser Val Phe Cys Leu His Lys Thr Asn Cys	
	20	30
	Thr Val Ala Glu Ile Tyr Leu Gly Asn Ile Ala Ser Ala Asp Leu Ile	
	35	45
40	Ile Ala Cys Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe	
	50	60
	Asp Trp Leu Phe Gly Glu Val Leu Cys Arg Val Val Asn Leu Tyr Met	
	65	80
45	Asn Leu Tyr Ser Ser Ile Cys Phe Leu Val Ser Ile Asp Arg Tyr Leu	
	85	95
	Ala Leu Val Lys Thr Met Ser Asn Leu Arg Trp Ala Lys Leu Tyr Ser	
	100	110

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Leu Val Ile Trp Ser Cys Thr Leu Leu Leu Ser Ser Pro Met Leu Val
 115 120 125
 Phe Arg Thr Met Tyr Arg Glu Glu Gly His Asn Val Thr Cys Val Ile
 130 135 140
 5 Val Tyr Pro Ser Arg Ser Trp Glu Val Phe Leu Leu Asn Leu Val Gly
 145 150 155 160
 Phe Leu Leu Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Arg Ile Met
 165 170 175
 10 Val Leu Arg Asn Asn Glu Met Lys Lys Phe Lys Glu Val Gln Thr Glu
 180 185 190
 Lys Lys Ala Thr Val Leu Val Ile Ala Val Leu Gly Leu Phe Val Leu
 195 200 205
 Cys Trp Phe Pro Phe Gln Ile Ser Thr Phe Leu Asp Thr Leu Leu Arg
 210 215 220
 15 Leu Gly Val Leu Ser Gly Cys Trp Asn Glu Arg Ala Val Asp Ile Val
 225 230 235 240
 Arg Gln Ile Ser Ser Tyr Val Ala Tyr Ser Asn Ser Cys Leu Asn Pro
 245 250 255
 20 Leu Val Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu
 260 265 270
 Val Tyr Gln Ala Ile Cys Arg Lys Gly Gly Cys Met Gly Glu Ser Val
 275 280 285
 Leu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln
 290 295 300
 25 Ile His Lys Leu Gln Asp Trp Ala Gly Asn Lys Gln
 305 310 315
 (2) INFORMATION FOR SEQ ID NO:47:
 (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 347 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
 35 Ile Leu Leu Val Val Ile Ile Cys Gly Leu Gly Ile Val Gly Asn Ile
 1 5 10 15
 Met Val Val Leu Val Val Met Arg Thr Thr Pro Thr Asn Cys Tyr Leu
 20 25 30
 40 Val Ser Ile Ala Val Ala Asp Leu Met Val Leu Val Ala Ala Gly Leu
 35 40 45
 Pro Asn Ile Thr Asp Ser Ile Tyr Gly Ser Trp Val Tyr Gly Tyr Val
 50 55 60
 Gly Cys Leu Cys Ile Thr Tyr Leu Gln Tyr Leu Gly Ile Asn Ala Ser
 65 70 75 80
 45 Ser Cys Ser Ile Thr Ala Phe Thr Ile Glu Arg Tyr Ile Ala Ile Cys
 85 90 95
 His Pro Ile Lys Ala Gln Phe Leu Cys Thr Phe Ser Arg Ala Lys Lys

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	100	105	110
	Ile Ile Ile Phe Val Trp Ala Phe Thr Ser Ile Tyr Leu Phe Leu Leu		
	115	120	125
5	Asp Ile Asn Ile Ser Thr Tyr Lys Asn Ala Val Val Val Ser Cys Gly		
	130	135	140
	Tyr Lys Ile Ser Arg Asn Tyr Tyr Ser Pro Ile Tyr Leu Met Asp Phe		
	145	150	155
	Gly Val Phe Tyr Val Val Pro Leu Ile Ala Thr Val Leu Tyr Gly Phe		
	165	170	175
10	Ile Ala Arg Ile Leu Phe Leu Asn Pro Ile Pro Ser Asp Pro Lys Glu		
	180	185	190
	Asn Ser Lys Met Trp Lys Asn Asp Ser Ile His Gln Asn Lys Asn Leu		
	195	200	205
15	Asn Leu Asn Ala Ser Ser Arg Lys Gln Val Thr Ile Asn Leu Ala Val		
	210	215	220
	Val Val Ile Leu Phe Ala Leu Leu Trp Asn Thr Tyr Arg Thr Leu Val		
	225	230	235
	Val Val Asn Ser Phe Leu Ser Ser Pro Phe Gln Glu Asn Trp Lys Leu		
	245	250	255
20	Leu Lys Cys Arg Ile Cys Ile Tyr Leu Asn Ser Ala Ile Asn Pro Val		
	260	265	270
	Ile Tyr Asn Ile Met Ser Gln Lys Arg Phe Ala Ala Phe Arg Lys Leu		
	275	280	285
25	Cys Asn Cys Lys Gln Lys Pro Thr Glu Lys Ala Ala Asn Tyr Ser Val		
	290	295	300
	Ala Leu Asn Tyr Ser Val Ile Lys Glu Ser Asp Arg Phe Ser Thr Glu		
	305	310	315
	Leu Glu Asp Ile Thr Val Thr Asp Thr Tyr Val Ser Thr Thr Lys Val		
	325	330	335
30	Ser Phe Asp Asp Thr Cys Ile Ala Ser Glu Asn		
	340	345	

(2) INFORMATION FOR SEQ ID NO:48:

	(i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 341 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: peptide
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
	Leu Ala Leu Trp Ala Thr Ala Tyr Leu Ala Leu Val Leu Val Ala Val
	1 5 10 15
	Thr Gly Asn Ala Ile Val Ile Trp Ile Ile Leu Ala His Arg Arg Met
	20 25 30
45	Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Ile Ala Leu Ala Asp Leu
	35 40 45
	Leu Asn Ala Ala Phe Asn Phe Val Tyr Ala Ser His Asn Ile Trp Tyr

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	50	55	60
	Phe Gly Arg Ala Phe Cys Tyr Phe Gln Asn Leu Phe Pro Ile Thr Ala 65 70 75 80		
5	Met Phe Val Ser Ile Tyr Ser Met Thr Ala Ile Ala Ala Asp Arg Tyr 85 90 95		
	Met Ala Ile Val His Pro Phe Gln Pro Arg Leu Ser Ala Pro Ser Thr 100 105 110		
	Lys Ala Val Ile Ala Gly Ile Trp Leu Val Ala Ile Lys Leu Ala Phe 115 120 125		
10	Pro Gln Cys Phe Tyr Ser Thr Val Thr Met Gln Gly Ala Thr Lys Cys 130 135 140		
	Val Val Ala Trp Pro Glu Asp Ser Gly Gly Lys Thr Leu Leu Leu Tyr 145 150 155 160		
15	His Leu Val Val Ile Ala Leu Ile Tyr Phe Leu Pro Ile Ala Leu Ala 165 170 175		
	Tyr Ser Val Ile Gly Leu Thr Leu Trp Arg Arg Ala Val Pro Gly His 180 185 190		
	Gln Ala His Gly Ala Asn Leu Arg His Leu Gln Ala Lys Lys Lys Phe 195 200 205		
20	Val Lys Thr Met Val Leu Val Val Val Thr Phe Ala Ile Cys Trp Leu 210 215 220		
	Pro Tyr His Leu Tyr Phe Ile Leu Gly Ser Phe Gln Glu Asp Ile Tyr 225 230 235 240		
25	Cys His Lys Phe Ile Gln Gln Val Tyr Leu Ala Leu Phe Trp Leu Ala 245 250 255		
	Met Ser Ser Thr Met Tyr Asn Pro Ile Ile Tyr Cys Cys Leu Asn His 260 265 270		
	Arg Phe Arg Ser Gly Phe Arg Leu Ala Phe Arg Cys Cys Pro Trp Val 275 280 285		
30	Thr Pro Thr Lys Glu Asp Lys Leu Glu Leu Thr Pro Thr Thr Ser Leu 290 295 300		
	Ser Thr Arg Val Asn Arg Cys His Thr Lys Glu Thr Leu Phe Met Ala 305 310 315 320		
35	Gly Asp Thr Ala Pro Ser Glu Ala Thr Ser Gly Glu Ala Gly Arg Pro 325 330 335		
	Gln Asp Gly Ser Gly 340		

(2) INFORMATION FOR SEQ ID NO:49:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ile Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Arg Ser Val
1 5 10 15

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	Val	Gly	Asn	Val	Val	Val	Ile	Trp	Ile	Ile	Leu	Ala	His	Lys	Arg	Met
			20						25					30		
	Arg	Thr	Val	Thr	Asn	Tyr	Phe	Leu	Val	Asn	Ile	Ala	Phe	Ala	Phe	Ala
			35					40					45			
5	Leu	Asn	Thr	Trp	Asn	Phe	Thr	Tyr	Ala	Val	His	Asn	Val	Trp	Tyr	Tyr
		50				55						60				
	Gly	Leu	Phe	Tyr	Cys	Lys	Phe	His	Asn	Phe	Phe	Pro	Ile	Ala	Ala	Leu
	65				70						75					80
10	Phe	Ala	Ser	Ile	Tyr	Ser	Met	Thr	Ala	Val	Ala	Phe	Asp	Arg	Tyr	Leu
				85						90					95	
	Ile	Ile	His	Pro	Leu	Gln	Pro	Arg	Leu	Ser	Ala	Thr	Ala	Thr	Lys	Val
				100					105					110		
	Val	Ile	Phe	Val	Ile	Trp	Val	Ile	Ala	Leu	Leu	Leu	Ala	Ser	Pro	Gln
			115					120					125			
15	Gly	Tyr	Tyr	Ser	Thr	Thr	Glu	Leu	Ser	Arg	Val	Val	Cys	Met	Ile	Glu
		130					135					140				
	Trp	Pro	Glu	His	Pro	Asn	Arg	Thr	Tyr	Glu	Lys	Ala	Tyr	His	Ile	Cys
	145					150					155					160
20	Val	Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Leu	Val	Ile	Gly	Tyr	Ala
				165					170					175		
	Tyr	Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp
				180					185					190		
	Ser	Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val
			195					200					205			
25	Lys	Met	Ile	Cys	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro
		210					215					220				
	Phe	His	Val	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu
	225					230					235					240
30	Lys	Lys	Phe	Ile	Gln	Gln	Val	Tyr	Ile	Ala	Ser	Met	Trp	Leu	Ala	Met
				245						250					255	
	Ser	Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg
				260					265					270		
	Phe	Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser
			275					280					285			
35	Ala	Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Ile	Lys	Ser	Thr	Arg	Tyr	Leu
		290					295					300				
	Gln	Thr	Leu	Ser	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile
	305					310					315					320
40	Ser	Thr	Val	Val	Gly	Ala	His	Glu	Glu	Glu	Pro	Glu	Glu	Gly	Pro	Lys
				325						330					335	
	Ala	Thr	Pro	Ser												
				340												

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 336 amino acids
 (B) TYPE: amino acid

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(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

5	Ile	Ala	Leu	Trp	Ser	Leu	Ala	Tyr	Gly	Leu	Val	Val	Ala	Val	Ala	Val	1	5	10	15
	Phe	Gly	Asn	Leu	Ile	Val	Ile	Trp	Ile	Ile	Leu	Ala	His	Lys	Arg	Met	20	25	30	
10	Arg	Thr	Val	Thr	Asn	Tyr	Phe	Leu	Val	Asn	Leu	Ala	Phe	Ser	Asp	Ala	35	40	45	
	Ser	Val	Ala	Ala	Phe	Asn	Thr	Leu	Ile	Asn	Phe	Ile	Tyr	Gly	Leu	His	50	55	60	
	Ser	Glu	Trp	Tyr	Phe	Gly	Ala	Asn	Tyr	Cys	Arg	Phe	Gln	Asn	Phe	Phe	65	70	75	80
15	Pro	Ile	Thr	Ala	Val	Phe	Ala	Ser	Ile	Tyr	Ser	Met	Ala	Ile	Ala	Val	85	90	95	
	Asp	Arg	Tyr	Met	Ala	Ile	Ile	Asp	Pro	Leu	Lys	Pro	Arg	Leu	Ser	Ala	100	105	110	
20	Thr	Ala	Thr	Lys	Ile	Val	Ile	Gly	Ser	Ile	Trp	Ile	Leu	Ala	Phe	Leu	115	120	125	
	Leu	Ala	Phe	Pro	Gln	Cys	Leu	Tyr	Ser	Lys	Ile	Leu	Gly	Arg	Thr	Leu	130	135	140	
	Cys	Tyr	Val	Trp	Pro	Glu	Gly	Pro	Lys	Gln	His	Phe	Thr	Tyr	His	Ile	145	150	155	160
25	Ile	Val	Ile	Ile	Leu	Val	Tyr	Cys	Phe	Pro	Leu	Leu	Ile	Leu	Thr	Tyr	165	170	175	
	Thr	Ile	Val	Gly	Ile	Thr	Leu	Trp	Gly	Gly	Glu	Ile	Pro	Gly	Asp	Thr	180	185	190	
30	Cys	Asp	Lys	Tyr	His	Glu	Gln	Leu	Lys	Ala	Lys	Arg	Lys	Val	Val	Met	195	200	205	
	Asn	Ile	Val	Val	Val	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Tyr	His	Val	210	215	220	
	Tyr	Phe	Ile	Leu	Thr	Ala	Ile	Tyr	Gln	Gln	Leu	Asn	Arg	Trp	Lys	Tyr	225	230	235	240
35	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ser	Phe	Trp	Leu	Ala	Met	Ser	Ser	Thr	245	250	255	
	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Lys	Arg	Phe	Arg	Ala	260	265	270	
40	Gly	Phe	Lys	Arg	Ala	Phe	Arg	Trp	Cys	Pro	Phe	Ile	Gln	Val	Ser	Ser	275	280	285	
	Tyr	Asp	Glu	Leu	Glu	Leu	Lys	Thr	Thr	Arg	Phe	His	Pro	Thr	Arg	Gln	290	295	300	
	Ser	Ser	Leu	Tyr	Thr	Val	Ser	Phe	Met	Ser	Val	Thr	Val	Leu	Phe	Asp	305	310	315	320
45	Pro	Asn	Asp	Gly	Asp	Pro	Thr	Lys	Ser	Ser	Arg	Lys	Lys	Arg	Ala	Val	325	330	335	

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(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

10	Met	Ile	Pro	Thr	Leu	Tyr	Ser	Ile	Ile	Phe	Val	Val	Gly	Ile	Phe	Gly
	1				5					10					15	
	Asn	Ser	Leu	Val	Val	Ile	Val	Ile	Tyr	Phe	Tyr	Met	Lys	Leu	Lys	Thr
				20					25					30		
	Tyr	Ala	Ser	Val	Phe	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Cys	Phe
				35				40					45			
15	Leu	Leu	Thr	Leu	Pro	Leu	Trp	Ala	Val	Tyr	Thr	Leu	Tyr	Arg	Trp	Pro
		50					55					60				
	Phe	Gly	Asn	Tyr	Leu	Cys	Lys	Ile	Ala	Ser	Ala	Ser	Val	Ser	Phe	Asn
	65					70				75						80
20	Leu	Tyr	Ala	Ser	Val	Phe	Leu	Leu	Thr	Cys	Leu	Ser	Ile	Asp	Arg	Tyr
					85					90					95	
	Leu	Ala	Ile	Val	His	Pro	Met	Lys	Ser	Arg	Leu	Arg	Arg	Leu	Val	Ala
				100					105					110		
	Lys	Val	Thr	Cys	Ile	Ile	Ile	Trp	Leu	Leu	Ala	Gly	Ile	Ala	Ser	Leu
			115					120					125			
25	Pro	Thr	Ile	Ile	His	Arg	Asn	Phe	Phe	Ile	Glu	Asn	Thr	Asn	Ile	Thr
		130					135					140				
	Val	Cys	Ala	Phe	His	Tyr	Glu	Ser	Gln	Asn	Ser	Thr	Leu	Pro	Val	Gly
	145					150				155						160
30	Leu	Gly	Leu	Thr	Lys	Asn	Ile	Leu	Gly	Phe	Leu	Phe	Pro	Phe	Leu	Ile
					165					170					175	
	Ile	Leu	Thr	Ser	Tyr	Thr	Leu	Ile	Trp	Lys	Thr	Leu	Lys	Lys	Ala	Tyr
			180						185					190		
	Glu	Ile	Gln	Lys	Asn	Lys	Pro	Arg	Lys	Asp	Asp	Ile	Phe	Lys	Ile	Ile
			195					200					205			
35	Ile	Ala	Ile	Val	Leu	Phe	Phe	Phe	Phe	Ser	Trp	Val	Pro	His	Asn	Ile
		210					215					220				
	Phe	Thr	Phe	Met	Val	Leu	Ile	Gln	Leu	Gly	Leu	Ile	Arg	Asp	Cys	Lys
	225					230				235					240	
40	Ile	Glu	Asp	Ile	Val	Asp	Thr	Ala	Met	Pro	Ile	Thr	Ile	Cys	Leu	Ala
					245					250					255	
	Tyr	Phe	Gln	Gln	Asn	Leu	Asn	Pro	Leu	Phe	Tyr	Gly	Phe	Leu	Gly	Lys
				260					265					270		
	Lys	Phe	Lys	Lys	Tyr	Phe	Leu	His	Ala	Leu	Leu	Lys	Tyr	Ile	Pro	Pro
			275					280					285			
45	Lys	Ala	Lys	Ser	His	Ser	Asn	Leu	Ser	Thr	Lys	Met	Ser	Thr	Leu	Ser
		290					295					300				

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Tyr Arg Pro Ser Glu Gln Gly Asn Ser Ser Thr Lys Lys Pro Ala Pro
 305 310 315 320

Cys Ile Glu Val Glu
 325

5 (2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Val His Trp Val Ile Met Ser Ile Ser Pro Val Gly Phe Val Glu
 1 5 10 15

Asn Gly Ile Leu Leu Trp Phe Leu Cys Phe Phe Thr Val Tyr Thr His
 20 25 30

Leu Ser Ile Ala Asp Ile Ser Leu Leu Phe Cys Ile Phe Ile Leu Ser
 35 40 45

Ile Asp Tyr Ala Leu Asp Tyr Glu Leu Ser Ser Gly His Tyr Tyr Thr
 50 55 60

Ile Val Thr Leu Ser Val Thr Phe Leu Phe Gly Tyr Asn Thr Gly Leu
 65 70 75 80

Tyr Leu Leu Thr Ala Ile Ser Val Glu Arg Cys Leu Ser Val Leu Tyr
 85 90 95

Pro Ile Trp Tyr Arg Cys His Arg Pro Lys Tyr Gln Ser Ala Leu Val
 100 105 110

Cys Ala Leu Leu Trp Ala Leu Ser Cys Leu Val Thr Thr Met Tyr Val
 115 120 125

Met Cys Ile Asp Arg Phe Glu Glu Ser His Ser Arg Asn Asp Cys Arg
 130 135 140

Ala Val Ile Ile Phe Ile Ala Ile Leu Ser Phe Leu Val Phe Thr Pro
 145 150 155 160

Ser Val Ser Ser Thr Ile Leu Val Val Lys Ile Arg Lys Asn Thr Trp
 165 170 175

Ala Ser His Ser Ser Lys Leu Tyr Ile Val Ile Met Val Thr Ile Ile
 180 185 190

Ile Phe Leu Ile Phe Ala Met Pro Met Arg Leu Leu Tyr Leu Leu Tyr
 195 200 205

Tyr Glu Tyr Trp Ser Thr Phe Gly Asn Leu His His Ile Ser Leu Leu
 210 215 220

Phe Ser Thr Ile Asn Ser Ser Ala Asn Pro Phe Ile Tyr Phe Phe Val
 225 230 235 240

Gly Ser Ser Lys Lys Lys Arg Phe Lys Glu Ser Leu Lys Val Val Leu
 245 250 255

Thr Arg Ala Phe Lys Asp Glu Met Gln Pro Arg Arg Gln Lys Asp Asn
 260 265 270

Cys Asn Thr Val Thr Val Glu Thr Val Val

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275

280

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

10 Tyr Asp Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile
 1 5 10 15
 Met Gly Asn Val Met Thr Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys
 20 25 30
 15 Leu Thr Val Pro Arg Phe Ile Met Asn Leu Ser Phe Ala Asp Phe Cys
 35 40 45
 Met Leu Tyr Leu Leu Leu Ile Ala Ser Val Asp Ser Gln Thr Lys Gly
 50 55 60
 Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys Ser
 65 70 75 80
 20 Thr Ala Gly Phe Phe Thr Val Leu Ala Ser Glu Leu Ser Val Tyr Thr
 85 90 95
 Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala Ile
 100 105 110
 25 His Ile Asp Gln Lys Leu Arg Leu Arg His Ala Ile Leu Ile Met Leu
 115 120 125
 Gly Gly Trp Leu Phe Ser Ser Leu Ile Ala Met Leu Pro Leu Val Cys
 130 135 140
 Val Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met Val Glu Thr
 145 150 155 160
 30 Thr Leu Ser Gln Val Tyr Ile Leu Thr Ile Leu Ile Leu Asn Val Val
 165 170 175
 Ala Phe Leu Ile Ile Cys Ala Cys Tyr Ile Lys Ile Tyr Phe Ala Val
 180 185 190
 35 Arg Asn Pro Glu Ile Met Ala Thr Asn Lys Asp Thr Lys Ile Ala Leu
 195 200 205
 Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Pro Ile Ser Phe Phe
 210 215 220
 Ala Ile Ser Ala Ala Phe Lys Val Pro Leu Ile Val Thr Asn Ser Lys
 225 230 235 240
 40 Val Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala Asn Pro Phe
 245 250 255
 Leu Tyr Ala Ile Phe Thr Lys Thr Phe Gln Arg Asp Phe Phe Ile Leu
 260 265 270
 45 Ser Lys Phe Cys Cys Lys Arg Arg Ala Asp Ile Tyr Arg Arg Lys Asp
 275 280 285
 Phe Ser Ala Tyr Thr Ser Asn Cys Lys Lys Gly Phe Thr Gly Ser Asn
 290 295 300

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Lys Pro Ser Gln Ser Thr Leu Lys Leu Ser Thr Leu His Cys Gln Gly
305 310 315 320

Thr Ala Leu Leu Asp Lys Arg Arg Tyr Thr Glu Cys
325 330

5 (2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Tyr Lys Phe Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu
1 5 10 15

Leu Gly Asn Val Phe Val Leu Leu Ile Leu Leu Thr Ser His Tyr Lys
20 25 30

Leu Asn Val Pro Arg Phe Ile Met Asn Ile Ala Phe Ala Asp Phe Cys
35 40 45

Met Met Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser
50 55 60

Glu Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn
65 70 75 80

Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr
85 90 95

Leu Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met
100 105 110

Arg Leu Asp Arg Lys Ile Arg Leu Arg His Ala Cys Ala Ile Met Val
115 120 125

Gly Gly Trp Val Cys Cys Phe Leu Leu Ala Leu Leu Pro Leu Val Gly
130 135 140

Ile Ser Ser Tyr Ala Lys Val Ser Ile Cys Leu Pro Met Thr Glu Thr
145 150 155 160

Pro Leu Ala Leu Ala Tyr Ile Val Phe Val Leu Thr Leu Asn Ile Val
165 170 175

Ala Phe Val Ile Val Cys Cys Cys Tyr Val Lys Ile Tyr Ile Thr Val
180 185 190

Arg Asn Pro Gln Tyr Asn Pro Gly Asp Lys Asp Thr Lys Ile Ala Lys
195 200 205

Arg Met Ala Val Leu Ile Phe Thr Asp Phe Ile Cys Met Ala Pro Ile
210 215 220

Ser Phe Tyr Ala Leu Ser Ala Ile Leu Asn Lys Pro Leu Ile Thr Val
225 230 235 240

Ser Asn Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro Leu Asn Ser Cys
245 250 255

Ala Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp
260 265 270

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Val Phe Ile Leu Leu Ser Lys Phe Gly Ile Cys Lys Arg Gln Ala Gln
 275 280 285

Ala Tyr Arg Gly Gln Arg Val Pro Pro Lys Asn Ser Thr Asp Ile Gln
 290 295 300

5 Val Gln Lys Val Thr His Asp Met Arg Gln Gly Ala Leu Asn Met Glu
 305 310 315 320

Asp Val Val Glu Leu Ile Glu Asn Ser His Leu Thr Pro Lys Lys Gln
 325 330 335

(2) INFORMATION FOR SEQ ID NO:55:
 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
 Tyr Asn Ile Leu Arg Val Leu Ile Trp Phe Ile Ser Ile Leu Ala Ile
 1 5 10 15

Thr Gly Asn Ile Ile Val Leu Val Ile Leu Thr Thr Ser Gln Tyr Lys
 20 20 25 30

Leu Thr Val Pro Arg Phe Leu Met Asn Ile Ala Phe Ala Asp Leu Cys
 35 40 45

Ile Gly Ile Tyr Leu Leu Leu Ile Ala Ser Val Asp Ile His Thr Lys
 50 55 60

25 Ser Gln Tyr His Asn Tyr Ala Ile Asp Trp Gln Arg Gly Ala Gly Cys
 65 70 75 80

Asp Ala Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr
 85 90 95

30 Thr Leu Thr Ala Ile Thr Leu Glu Arg Trp His Thr Ile Thr His Ile
 100 105 110

Met Gln Ile Asp Cys Lys Val Gln Leu Arg His Ala Ala Ser Val Met
 115 120 125

Val Met Gly Trp Ile Phe Ala Phe Ala Ala Ala Leu Phe Pro Ile Phe
 130 135 140

35 Gly Ile Ser Ser Tyr Met Lys Val Ser Ile Cys Leu Pro Leu Ile Asp
 145 150 155 160

Ser Pro Leu Ser Gln Leu Tyr Val Met Ser Leu Leu Val Leu Asn Val
 165 170 175

40 Leu Ala Phe Val Val Ile Cys Gly Cys Tyr Thr His Ile Tyr Leu Thr
 180 185 190

Val Arg Asn Pro Asn Ile Val Ser Ser Ser Asp Thr Arg Ile Ala
 195 200 205

Lys Arg Met Leu Ile Phe Thr Asp Phe Leu Leu Pro Ile Ser Phe Phe
 210 215 220

45 Ala Ile Ser Ala Ser Leu Lys Val Pro Leu Ile Thr Val Ser Lys Ala
 225 230 235 240

Lys Ile Leu Leu Val Leu Phe His Pro Ile Asn Ser Cys Ala Asn Pro

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	245	250	255
	Phe Leu Tyr Ala Ile Phe Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile		
	260	265	270
5	Leu Leu Ser Lys Cys Gly Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg		
	275	280	285
	Thr Glu Thr Ser Ser Thr Val His Asn Thr His Pro Arg Asn Gly His		
	290	295	300
	Cys Ser Ser Ala Pro Arg Val Thr Ser Gly Ser Ser Arg Tyr Ile Leu		
	305	310	315
10	Val Pro Leu Ser Leu Gln Asn		
	325		

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

20	Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile Val Leu Gly Phe Pro	1	5	10	15
	Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln His Lys Lys Leu Arg	20	25	30	
25	Thr Pro Ile Asn Tyr Ile Leu Leu Asn Leu Ala Val Ala Asp Leu Phe	35	40	45	
	Met Val Leu Gly Gly Phe Thr Ser Thr Leu Tyr Thr Ser Leu His Gly	50	55	60	
	Tyr Phe Val Phe Gly Pro Thr Gly Cys Asn Leu Glu Gly Phe Phe Ala	65	70	75	80
30	Thr Leu Gly Gly Glu Ile Ala Leu Trp Ser Leu Trp Leu Ala Ile Glu	85	90	95	
	Arg Tyr Val Val Val Cys Lys Pro Met Ser Asn Phe Arg Phe Gly Glu	100	105	110	
35	Asn His Ala Ile Met Gly Val Ala Phe Thr Trp Val Met Ala Leu Ala	115	120	125	
	Cys Ala Ala Pro Pro Ile Ala Gly Trp Ser Arg Tyr Ile Pro Glu Gly	130	135	140	
	Leu Gln Cys Ser Cys Gly Ile Asp Tyr Tyr Thr Leu Lys Pro Glu Val	145	150	155	160
40	Asn Asn Glu Ser Phe Val Ile Tyr Met Phe Val Val His Phe Thr Ile	165	170	175	
	Pro Leu Ile Ile Phe Phe Cys Tyr Gly Gln Leu Val Phe Thr Val Lys	180	185	190	
45	Glu Ala Ala Ala Gln Gln Gln Glu Ser Ala Thr Thr Gln Lys Ala Glu	195	200	205	
	Lys Glu Val Thr Arg Met Val Ile Ile Met Val Ile Ala Phe Leu Ile	210	215	220	

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Cys Trp Val Pro Tyr Ala Ser Val Ala Phe Tyr Ile Phe Thr His Gln
 225 230 235 240
 Gly Ser Asn Phe Gly Pro Ile Phe Met Arg Ile Pro Ala Phe Phe Ala
 245 250 255
 5 Lys Ser Ala Ala Ile Tyr Asn Pro Val Ile Tyr Ile Ile Phe Asn Lys
 260 265 270
 Gln Phe Arg Asn Cys Met Leu Gln Leu Ile Cys Cys Gly Lys Asn Pro
 275 280 285
 10 Leu Gly Asp Asp Glu Ala Ser Ala Thr Val Ser Lys Arg Glu Thr Ser
 290 295 300
 Gln Val Ala Pro Ala
 305

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 297 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Ile Phe Val Val Ile Ala Ser Val Phe Thr Asn Gly Leu Val Leu
 1 5 10 15
 Ala Ala Thr Met Lys Phe Lys Lys Leu Pro His Pro Ile Asn Trp Ile
 20 25 30
 25 Leu Val Asn Leu Ala Val Ala Asp Ile Ala Gly Thr Val Ile Ala Ser
 35 40 45
 Thr Ile Ser Val Val Asn Gln Val Tyr Gly Tyr Phe Val Leu Gly His
 50 55 60
 30 Pro Met Cys Val Leu Glu Gly Tyr Thr Val Ser Leu Cys Gly Ile Thr
 65 70 75 80
 Gly Leu Trp Ser Leu Ala Ile Ile Ser Trp Glu Arg Trp Met Val Val
 85 90 95
 Cys Lys Pro Phe Gly Asn Val Arg Phe Asp Ala Lys Ile Ala Ile Val
 100 105 110
 35 Gly Ile Ala Phe Ser Trp Ile Trp Ala Ala Val Trp Thr Ala Pro Pro
 115 120 125
 Ile Phe Gly Trp Ser Arg Tyr Trp Pro His Gly Leu Lys Thr Ser Cys
 130 135 140
 40 Gly Pro Asp Val Phe Ser Gly Ser Ser Tyr Pro Gly Val Gln Ser Leu
 145 150 155 160
 Leu Cys Ile Thr Pro Leu Ser Ile Ile Val Leu Cys Tyr Leu Gln Val
 165 170 175
 Trp Thr Ala Ile Arg Ala Val Ala Lys Gln Gln Lys Glu Ser Glu Ser
 180 185 190
 45 Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Trp Val Met Val Leu
 195 200 205
 Ala Phe Cys Phe Cys Trp Gly Pro Tyr Ala Phe Phe Ala Cys Phe Ala

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	210		215		220	
	Ala Ala Asn Pro Gly Tyr	Pro Phe His Pro	Leu Met Ala Ala Leu Pro			
	225	230	235	240		
5	Ala Phe Phe Ala Lys Ser	Ala Thr Ile Tyr	Asn Pro Val Ile Tyr	Val		
	245	250	255			
	Phe Met Asn Arg Gln Phe	Arg Asn Cys Ile	Leu Gln Leu Phe Gly Lys			
	260	265	270			
	Lys Val Asp Asp Gly Ser	Glu Leu Ser Ser	Ala Ser Lys Thr Glu Val			
	275	280	285			
10	Ser Ser Val Ser Ser Val	Ser Pro Ala				
	290	295				

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

20	Arg Cys Phe Val Val Thr	Ala Ser Val Phe Thr	Asn Gly Leu Val Leu
	1	5	10
	Ala Ala Thr Met Lys Phe	Lys Lys Leu Arg His	Pro Leu Asn Trp Ile
	20	25	30
25	Leu Val Asn Ile Ala Val	Ala Asp Ile Ala Gly Thr	Val Ile Ala Ser
	35	40	45
	Thr Ile Ser Ile Val Asn	Gln Val Ser Gly Tyr Phe	Val Leu Gly His
	50	55	60
	Pro Met Cys Val Leu Glu	Gly Tyr Thr Val Ser	Leu Cys Gly Ile Thr
	65	70	75
30	Gly Leu Trp Ser Leu Ala	Ile Ile Ser Trp Glu Arg	Trp Leu Trp Cys
	85	90	95
	Lys Pro Phe Gly Asn Val	Arg Phe Asp Ala Lys Ile	Ala Ile Val Gly
	100	105	110
35	Ile Ala Phe Ser Trp Ile	Trp Ser Ala Val Trp Thr	Ala Pro Pro Ile
	115	120	125
	Phe Gly Trp Ser Arg Tyr	Trp Pro His Gly Leu Lys	Thr Ser Cys Gly
	130	135	140
	Pro Asp Val Phe Ser Gly	Ser Ser Tyr Pro Gly Val	Gln Ser Leu Val
	145	150	155
40	Ile Met Val Thr Cys Cys	Ile Ile Pro Ile Ala Ile	Ile Leu Cys Tyr
	165	170	175
	Leu Gln Val Trp Leu Ala	Ile Arg Ala Val Ala Lys	Gln Gln Lys Glu
	180	185	190
45	Ser Glu Ser Thr Gln Lys	Ala Glu Lys Glu Val Thr	Arg Met Leu Phe
	195	200	205
	Ala Tyr Cys Val Cys Trp	Gly Pro Tyr Thr Phe Phe	Ala Cys Phe Ala
	210	215	220

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Ala Ala Asn Pro Gly Tyr Ala Phe His Pro Leu Met Ala Ala Leu Pro
 225 230 235 240

Ala Tyr Phe Ala Lys Ser Ala Thr Ile Tyr Asn Pro Val Ile Tyr Val
 245 250 255

5 Phe Met Asn Arg Gln Phe Arg Asn Cys Ile Leu Gln Leu Phe Gly Lys
 260 265 270

Lys Val Asp Asp Gly Ser Glu Leu Ser Ser Ala Ser Lys Thr Glu Val
 275 280 285

10 Ser Ser Val Ser Ser Val Ser Pro Ala
 290 295

(2) INFORMATION FOR SEQ ID NO:59:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

20 Gln Ala Ala Phe Met Gly Thr Val Phe Leu Ile Gly Phe Pro Leu Leu
 1 5 10 15

Val Ala Thr Leu Ala Tyr Lys Lys Leu Arg Gln Pro Asn Tyr Ile Leu
 20 25 30

Val Asn Val Ser Phe Gly Gly Phe Leu Leu Cys Ile Phe Ser Val Phe
 35 40 45

25 Pro Val Phe Val Ala Ser Cys Asn Gly Tyr Phe Val Phe Gly Arg His
 50 55 60

Val Cys Ala Leu Glu Gly Phe Leu Gly Thr Val Ala Gly Leu Val Thr
 65 70 75 80

30 Gly Trp Ser Leu Ala Phe Leu Ala Phe Glu Arg Tyr Ile Val Ile Cys
 85 90 95

Lys Pro Phe Gly Asn Phe Arg Phe Ser Ser Lys His Ala Leu Thr Val
 100 105 110

Val Ile Ala Thr Trp Thr Ile Gly Ile Gly Val Ser Ile Pro Pro Phe
 115 120 125

35 Phe Gly Trp Ser Arg Phe Ile Pro Glu Gly Leu Gln Cys Ser Cys Gly
 130 135 140

Pro Asp Lys Tyr Thr Val Gly Thr Lys Tyr Arg Ser Glu Ser Tyr Thr
 145 150 155 160

40 Trp Phe Leu Phe Ile Phe Cys Phe Ile Val Pro Leu Ser Leu Ile Cys
 165 170 175

Phe Ser Tyr Thr Gln Leu Leu Arg Ala Leu Lys Ala Val Ala Ala Gln
 180 185 190

Gln Gln Glu Ser Ala Thr Thr Gln Lys Ala Glu Arg Glu Val Ser Arg
 195 200 205

45 Met Val Val Val Met Val Gly Ser Phe Cys Val Cys Tyr Val Pro Tyr
 210 215 220

Ala Ala Phe Ala Met Tyr Met Val Asn Asn Arg Asn His Gly Leu Asp

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225 230 235 240
 Leu Arg Leu Val Arg Ile Pro Ser Phe Phe Ser Lys Ser Ala Cys Ile
 245 250 255
 5 Tyr Asn Pro Ile Ile Tyr Cys Phe Met Asn Lys Gln Phe Gln Ala Cys
 260 265 270
 Ile Met Met Val Cys Gly Lys Ala Met Met Glu Ser Asp Thr Cys Ser
 275 280 285
 Ser Gln Lys Thr Glu Val Ser Thr Val Ser Ser Thr Gln Val Gly Pro
 290 295 300
 10 Asn
 305
 (2) INFORMATION FOR SEQ ID NO:60:
 (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
 20 Leu Ile Tyr Gly Leu Phe Leu Ser Met Tyr Leu Val Thr Val Ile Gly
 1 5 10 15
 Asn Ile Ser Ile Ile Val Ala Ile Ile Ser Asp Pro Cys Leu His Thr
 20 25 30
 25 Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Val Asp Ile Cys Phe
 35 40 45
 Ile Ser Thr Thr Val Pro Val Asn Thr Gln Thr Gln Asn Asn Val Ile
 50 55 60
 Thr Tyr Ala Gly Cys Ile Thr Gln Ile Tyr Phe Phe Leu Leu Phe Val
 65 70 75 80
 30 Glu Leu Asp Asn Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Val
 85 90 95
 Ala Ile Cys His Pro Met His Tyr Thr Val Ile Met Asn Tyr Lys Leu
 100 105 110
 35 Cys Gly Phe Leu Val Leu Val Ser Trp Ile Val Ser Val Leu His Ala
 115 120 125
 Leu Phe Gln Ser Leu Ala Leu Pro Phe Cys Thr His Leu Glu Ile Pro
 130 135 140
 His Tyr Phe Cys Glu Pro Asn Gln Val Ile Gln Leu Thr Cys Ser Asp
 145 150 155 160
 40 Ala Phe Leu Asn Asp Leu Val Ile Tyr Phe Thr Leu Val Leu Leu Ala
 165 170 175
 Thr Val Pro Ile Ala Gly Ile Phe Tyr Ser Tyr Phe Ala Ile Ser Ser
 180 185 190
 45 Val His Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser
 195 200 205
 Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr Leu Ser Ser
 210 215 220

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Ala Ala Asn Asn Ser Leu Ser Ala Thr Ala Ser Val Met Tyr Thr Val
 225 230 235 240

Val Thr Pro Met Val Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp
 245 250 255

5 Val Lys Ser Val Leu Lys Lys Thr Leu Cys Glu Glu Val Ile Arg Ser
 260 265 270

Pro Pro Ser Leu Leu His Phe Phe Leu Val Leu Cys His Leu Pro Cys
 275 280 285

10 Phe Ile Phe Cys Tyr
 290

(2) INFORMATION FOR SEQ ID NO:61:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

20 Leu Leu Phe Leu Phe Leu Ile Met Tyr Leu Ala Thr Val Leu Gly
 1 5 10 15

Asn Leu Leu Ile Ile Leu Ala Ile Gly Gly Asp Ser Arg Leu His Thr
 20 25 30

Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Val Asp Val Cys Phe
 35 40 45

25 Ser Ser Thr Thr Val Pro Lys Val Leu Ala Asn His Ile Leu Gly Ser
 50 55 60

Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr Gln Leu Tyr Phe Leu Ala
 65 70 75 80

30 Val Phe Gly Asn Met Asp Asn Phe Leu Leu Ala Val Met Ser Tyr Asp
 85 90 95

Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Ile Arg Gln
 100 105 110

Leu Cys Val Leu Leu Val Val Gly Ser Trp Val Val Ala Asn Met Asn
 115 120 125

35 Cys Leu Leu His Ile Leu Ile Met Ala Arg Lys Ser Phe Cys Ala Asp
 130 135 140

Leu Pro His Phe Phe Cys Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys
 145 150 155 160

40 Ser Asp Thr His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val
 165 170 175

Val Met Val Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile
 180 185 190

Thr Cys Ala Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ser
 195 200 205

45 Phe Ser Thr Cys Cys Ser His Ile Ala Val Val Cys Leu Phe Tyr Gly
 210 215 220

Thr Val Ile Ala Val Tyr Phe Asn Pro Ser Ser Ser His Leu Ala Gly

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225 230 235 240
 Arg Asp Met Ala Ala Val Met Tyr Ala Val Val Thr Pro Met Ile
 245 250 255
 5 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Ser Asp Met Lys Ala Ala Leu
 260 265 270
 Arg Lys Val Leu Ala Met Arg Phe Pro Ser Lys Gln
 275 280

(2) INFORMATION FOR SEQ ID NO:62:
 (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
 Leu Leu Phe Leu Leu Phe Leu Val Met Tyr Leu Leu Thr Val Val Gly
 1 5 10 15
 Asn Leu Ala Ile Ile Ser Leu Val Gly Ala His Arg Cys Leu Gln Pro
 20 25 30
 20 His Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Phe Leu Glu Ile
 35 40 45
 Trp Phe Thr Thr Ala Cys Val Pro Lys Thr Leu Ala Thr Phe Ala Pro
 50 55 60
 25 Arg Gly Gly Val Ile Ser Leu Ala Gly Cys Ala Thr Lys Tyr Phe Val
 65 70 75 80
 Phe Ser Leu Gly Cys Thr Glu Tyr Phe Leu Leu Ala Val Met Ala Tyr
 85 90 95
 Asp Arg Tyr Leu Ala Ile Cys Leu Pro Leu Arg Tyr Gly Gly Ile Met
 100 105 110
 30 Arg Pro Gly Ile Ala Met Arg Leu Ala Leu Gly Ser Trp Leu Cys Gly
 115 120 125
 Phe Ser Ala Ile Thr Val Pro Ala Thr Leu Ile Ala Arg Leu Ser Phe
 130 135 140
 35 Cys Gly Ser Arg Val Ile Asn His Phe Phe Cys Asp Ile Ser Pro Trp
 145 150 155 160
 Ile Val Leu Ser Cys Thr Asp Thr Gln Val Val Glu Leu Val Ser Phe
 165 170 175
 Gly Ile Ala Phe Cys Val Ile Leu Gly Ser Cys Gly Ile Thr Leu Val
 180 185 190
 40 Ser Tyr Ala Lys Ile Pro Ser Ala Arg Gly Arg His Arg Ala Phe Ser
 195 200 205
 Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp Tyr Gly Ser Thr
 210 215 220
 45 Ile Phe Leu His Val Arg Thr Ser Val Glu Ser Ser Leu Asp Leu Thr
 225 230 235 240
 Lys Ala Ile Thr Val Leu Asn Thr Ile Val Thr Pro Val Leu Asn Pro

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245 250 255

Phe Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Arg
260 265 270

5 Thr Val Lys Gly Lys
275

(2) INFORMATION FOR SEQ ID NO:63:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

15 Leu Ile Phe Ala Leu Phe Leu Ser Met Tyr Leu Val Thr Val Leu Gly
1 5 10 15

Asn Leu Leu Ile Ile Met Ala Ile Ile Thr Gln Ser His Leu His Thr
20 20 25 30

Pro Met Tyr Phe Phe Leu Ser Phe Val Asp Ile Cys Phe Thr Ser Thr
35 40 45

20 Thr Ile Pro Leu Val Asn Ile Tyr Thr Gln Ser Lys Ser Ile Thr Tyr
50 55 60

Glu Asp Cys Ile Ser Leu Val Phe Ala Glu Leu Gly Asn Phe Leu Leu
65 70 75 80

25 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Xaa Cys His Pro Leu Cys
85 90 95

Tyr Thr Val Ile Val Asn His Arg Leu Cys Ile Leu Leu Leu Leu Leu
100 105 110

Ser Trp Val Ile Ser Ile Phe Arg Ala Phe Ile Gln Ser Leu Ile Val
115 120 125

30 Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
130 135 140

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Asn Phe Pro Ser
145 150 155 160

35 His Leu Ile Met Asn Leu Val Pro Val Met Leu Ala Ala Ile Ser Phe
165 170 175

Ser Gly Ile Leu Tyr Ser Tyr Phe Ser Ile Ser Thr Val Gln Gly Lys
180 185 190

Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Ile Val Ser Leu
195 200 205

40 Phe Tyr Ser Thr Gly Leu Gly Val Tyr Val Ser Ser Ala Val Val Gln
210 215 220

Ser Ser His Ser Ala Ala Ser Ala Ser Val Met Tyr Thr Val Val Pro
225 230 235 240

45 Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg
245 250 255

Ala Leu Glu Arg Leu Leu Glu Gly Asn Cys Lys Val His His Trp Thr
260 265 270

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Gly

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

1	Leu	Phe	Tyr	Ala	Leu	Phe	Leu	Val	Met	Tyr	Leu	Thr	Thr	Ile	Leu	Gly
					5					10					15	
	Asn	Leu	Leu	Ile	Ile	Val	Leu	Val	Gln	Leu	Asp	Ser	Gln	Leu	His	Thr
			20					25						30		
15	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ser	Asp	Leu	Cys	Phe
			35					40					45			
	Ser	Ser	Leu	Lys	Leu	Leu	Gln	Asn	Met	Arg	Ser	Gln	Asp	Thr	Ser	Ile
			50				55					60				
20	Pro	Tyr	Gly	Gly	Cys	Leu	Ala	Gln	Thr	Tyr	Phe	Phe	Met	Val	Phe	Gly
			65			70					75				80	
	Asp	Leu	Ser	Phe	Leu	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala
				85					90					95		
	Ile	Cys	Phe	Leu	Pro	His	Tyr	Thr	Ser	Ile	Met	Ser	Pro	Lys	Leu	Cys
			100					105						110		
25	Thr	Cys	Leu	Val	Leu	Leu	Leu	Trp	Met	Leu	Thr	Thr	Ser	His	Met	Met
			115					120					125			
	Thr	Leu	Leu	Ala	Ala	Arg	Leu	Ser	Phe	Cys	Glu	Asn	Asn	Trp	Leu	Asn
			130			135						140				
30	Phe	Phe	Cys	Asp	Leu	Phe	Val	Leu	Leu	Lys	Ile	Ala	Cys	Ser	Asp	Thr
			145			150					155				160	
	Tyr	Ile	Asn	Glu	Leu	Phe	Ile	Met	Ser	Thr	Leu	Leu	Ile	Ile	Ile	Pro
				165					170					175		
	Phe	Phe	Leu	Ile	Val	Met	Ser	Tyr	Ala	Lys	Val	Pro	Ser	Thr	Gln	Gly
			180					185						190		
35	Ile	Cys	Lys	Val	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser
			195					200				205				
	Leu	Phe	Tyr	Gly	Thr	Ile	Ile	Gly	Leu	Tyr	Leu	Cys	Pro	Ala	Gly	Asn
			210				215					220				
40	Asn	Ser	Thr	Val	Lys	Glu	Met	Val	Met	Ala	Met	Met	Tyr	Thr	Val	Val
			225			230					235				240	
	Thr	Pro	Met	Ile	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Leu
				245					250					255		
	Arg	Ala	Leu	Ile	Arg	Val	Ile	Cys	Ser	Met	Ile	Thr	Leu			
			260					265								

45 (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

5	Leu	Leu	Phe	Phe	Leu	Ser	Leu	Leu	Xaa	Tyr	Val	Leu	Val	Leu	Thr	Glu
	1			5					10					15		
	Asn	Met	Leu	Ile	Ile	Ile	Ala	Ile	Arg	Asn	His	Pro	Thr	Leu	His	Lys
			20					25						30		
10	Pro	Met	Tyr	Phe	Phe	Leu	Phe	Leu	Glu	Ile	Trp	Tyr	Val	Thr	Val	Thr
		35					40					45				
	Ile	Pro	Lys	Leu	Met	Gly	Phe	Ile	Gly	Ser	Lys	Glu	Asn	His	Gly	Gln
		50				55						60				
	Leu	Ile	Ser	Phe	Phe	Ala	Cys	Met	Thr	Gln	Leu	Tyr	Phe	Phe	Leu	Gly
	65				70					75						80
15	Leu	Gly	Cys	Thr	Glu	Cys	Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg
				85					90						95	
	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Ser	Ser
			100					105					110			
20	Arg	Ile	Glx	Val	Leu	Gly	Ser	Trp	Ala	Gly	Gly	Phe	Gly	Ile	Ser	Met
			115				120						125			
	Val	Lys	Val	Phe	Leu	Ile	Ser	Arg	Leu	Ser	Tyr	Cys	Gly	Pro	Asn	Thr
		130					135					140				
	Ile	Asn	His	Phe	Phe	Cys	Asp	Val	Ser	Pro	Leu	Leu	Asn	Leu	Ser	Cys
	145				150					155						160
25	Thr	Asp	Met	Ser	Thr	Ala	Glu	Leu	Thr	Asp	Phe	Val	Ile	Ala	Ile	Phe
				165					170						175	
	Ile	Leu	Leu	Gly	Pro	Leu	Ser	Val	Thr	Gly	Ala	Ser	Tyr	Met	Arg	Ile
			180					185						190		
30	Pro	Ser	Ala	Ala	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His
			195				200						205			
	Leu	Thr	Val	Val	Ile	Ile	Phe	Tyr	Ala	Ala	Ser	Ile	Phe	Ile	Tyr	Ala
		210				215						220				
	Arg	Pro	Lys	Ala	Leu	Ser	Ala	Phe	Thr	Asp	Asn	Lys	Leu	Val	Ser	Val
	225				230					235						240
35	Leu	Tyr	Ala	Val	Ile	Val	Pro	Leu	Phe	Asn	Pro	Ile	Ile	Tyr	Cys	Leu
				245					250						255	
	Arg	Asn	Gln	Asp	Val	Lys	Arg	Ala	Leu	Arg	Arg	Thr	Leu	His	Leu	Ala
			260					265					270			
40	Gln	Asp	Gln	Glu	Ala	Asn	Thr	Asn	Lys	Gly	Ser	Lys	Ile	Gly		
		275					280						285			

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

	Leu	Phe	Phe	Ala	Leu	Phe	Leu	Ile	Met	Tyr	Leu	Thr	Thr	Phe	Leu	Gly	
	1				5					10					15		
5	Asn	Leu	Leu	Ile	Val	Val	Leu	Val	Gln	Leu	Asp	Ser	His	Leu	His	Thr	
				20					25					30			
	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ser	Asp	Leu	Cys	Phe	
			35					40					45				
	Ser	Ser	Val	Thr	Met	Leu	Lys	Leu	Leu	Gln	Asn	Ile	Gln	Ser	Gln	Val	
			50				55					60					
10	Pro	Ser	Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Trp	Ile	Phe	Phe	Phe	Leu	Leu	
						70					75				80		
	Phe	Gly	Tyr	Leu	Gly	Asn	Phe	Leu	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	
					85					90					95		
15	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Leu	His	Tyr	Thr	Asn	Ile	Met	Ser	His	
				100					105					110			
	Lys	Leu	Cys	Thr	Cys	Leu	Leu	Leu	Val	Phe	Trp	Ile	Met	Arg	Ser	Ser	
			115					120					125				
	His	Ala	Met	Met	Ile	Thr	Leu	Ile	Ala	Ala	Arg	Leu	Ser	Phe	Cys	Glu	
		130					135					140					
20	Asn	Asn	Val	Leu	Leu	Asn	Phe	Phe	Cys	Asp	Leu	Phe	Val	Leu	Leu	Lys	
						150					155				160		
	Leu	Ala	Cys	Ser	Asp	Thr	Tyr	Val	Asn	Glu	Leu	Met	Ile	His	Ile	Met	
					165					170					175		
25	Glu	Val	Ile	Ile	Ile	Val	Ile	Pro	Phe	Val	Leu	Ile	Val	Ile	Ser	Tyr	
				180					185					190			
	Ala	Lys	Val	Pro	Ser	Thr	Gln	Ser	Ile	His	Lys	Val	Phe	Ser	Thr	Cys	
			195					200					205				
	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ile	Ile	Gly	
		210					215					220					
30	Leu	Tyr	Leu	Cys	Pro	Ser	Gly	Asp	Asn	Phe	Ser	Leu	Lys	Gly	Ser	Leu	
					230						235				240		
	Thr	Val	Val	Thr	Pro	Ile	Met	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	
					245					250					255		
35	Asp	Met	Lys	Gln	Ala	Leu	Ile	Arg	Val	Thr	Cys	Ser	Lys	Lys	Ile	Ser	
				260					265					270			
	Leu	Pro	Trp														

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Leu	Phe	Tyr	Ala	Leu	Phe	Leu	Ala	Met	Tyr	Leu	Thr	Thr	Leu	Leu	Gly
1				5					10					15	

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	Asn	Leu	Ile	Ile	Ile	Leu	Ile	Leu	Leu	Asp	Ser	His	Leu	His	Thr	
			20					25					30			
	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ala	Asp	Leu	Cys	Phe
			35					40					45			
5	Ser	Ser	Leu	Lys	Leu	Leu	Gln	Asn	Met	Gln	Ser	Gln	Val	Pro	Ser	Ile
		50					55					60				
	Pro	Tyr	Ala	Gly	Cys	Leu	Ala	Gln	Ile	Tyr	Phe	Phe	Leu	Phe	Phe	Gly
	65					70					75					80
10	Asp	Leu	Gly	Asn	Phe	Leu	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val
				85						90					95	
	Ala	Ile	Cys	Phe	Pro	Leu	His	Tyr	Met	Ser	Ile	Met	Ser	Pro	Lys	Ile
				100					105					110		
	Glx	Val	Ser	Leu	Val	Val	Leu	Ser	Trp	Val	Leu	Thr	Thr	Phe	His	Ala
			115					120					125			
15	Met	Leu	His	Thr	Leu	Ile	Met	Ala	Arg	Leu	Ser	Phe	Cys	Glu	Asp	Ser
		130					135					140				
	Val	Ile	Pro	His	Tyr	Phe	Cys	Asp	Met	Ser	Thr	Leu	Leu	Lys	Val	Ala
	145					150					155					160
20	Cys	Ser	Asp	Thr	His	Asp	Asn	Glu	Leu	Ala	Ile	Phe	Ile	Leu	Gly	Gly
				165						170					175	
	Pro	Ile	Val	Val	Leu	Pro	Phe	Leu	Leu	Ile	Ile	Val	Ser	Tyr	Ala	Arg
				180					185					190		
	Ile	Val	Ser	Ser	Ile	Phe	Lys	Val	Pro	Ser	Ser	Gln	Ser	Ile	His	Lys
			195					200					205			
25	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr
		210					215					220				
	Gly	Thr	Val	Ile	Gly	Leu	Tyr	Leu	Cys	Pro	Ser	Ala	Asn	Asn	Ser	Glu
	225					230					235					240
30	Val	Lys	Glu	Thr	Val	Met	Ser	Ile	Tyr	Thr	Met	Val	Pro	Met	Leu	Asn
				245						250					255	
	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Lys	Asp	Ala	Leu	Glu
				260					265					270		
	Lys	Ile	Met	Cys	Lys	Lys	Gln	Ile	Pro	Ser	Phe	Leu				
			275					280								
35	(2)	INFORMATION FOR SEQ ID NO:68:														
		(i) SEQUENCE CHARACTERISTICS:														
		(A) LENGTH: 277 amino acids														
		(B) TYPE: amino acid														
		(C) STRANDEDNESS: single														
40		(D) TOPOLOGY: linear														

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Tyr Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser
 35 40 45
 Val Thr Trp Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile
 50 55 60
 5 Ser Tyr Thr Gly Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Gly
 65 70 75 80
 Asp Trp Ser Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala
 85 90 95
 10 Ile Cys Phe Pro Leu Arg Tyr Thr Thr Ile Met Ser Thr Lys Phe Cys
 100 105 110
 Ala Ser Leu Val Leu Leu Leu Trp Met Leu Thr Met Arg His Ala Leu
 115 120 125
 Leu His Thr Leu Leu Ile Ala Arg Leu Ser Phe Cys Glu Asp Ser Val
 130 135 140
 15 Ile Leu His Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys
 145 150 155 160
 Ser Asp Ile Tyr Val Asn Glu Leu Met Ile Tyr Ile Leu Gly Gly Leu
 165 170 175
 20 Ile Ile Ile Ile Pro Phe Leu Leu Ile Val Met Ser Tyr Val Arg Ile
 180 185 190
 Phe Phe Ser Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile Tyr Lys Val
 195 200 205
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly
 210 215 220
 25 Thr Ile Phe Gly Ile Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val
 225 230 235 240
 Lys Glu Ile Leu Thr Val Val Thr Pro Met Ile Asn Pro Phe Ile Tyr
 245 250 255
 30 Ser Leu Arg Asn Arg Asp Trp Arg Ala Leu Ile Arg Val Ile Cys Thr
 260 265 270
 Lys Lys Ile Ser Leu
 275

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

40 Val Phe Tyr Ala Leu Phe Leu Ser Met Tyr Leu Thr Ile Val Leu Gly
 1 5 10 15
 Asn Leu Ile Ile Ile Ile Leu Ile His Leu Asp Ser His Leu His Thr
 20 25 30
 45 Pro Met Tyr Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe
 35 40 45

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Ser Ser Leu Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile
 50 55 60
 Pro Phe Ala Gly Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala
 65 70 75 80
 5 Asp Leu Glu Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val
 85 90 95
 Ala Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu
 100 105 110
 10 Cys Val Ser Leu Trp Leu Ser Trp Val Leu Thr Thr Phe His Ala Met
 115 120 125
 Leu His Thr Leu Ile Met Ala Arg Leu Ser Phe Cys Ala Asp Leu Pro
 130 135 140
 His Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp
 145 150 155 160
 15 Thr His Val Asn Glu Leu Val Ile Phe Leu Gly Leu Val Ile Val Ile
 165 170 175
 Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser Ile
 180 185 190
 20 Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser Thr Cys
 195 200 205
 Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly
 210 215 220
 Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Leu
 225 230 235 240
 25 Thr Val Val Thr Pro Leu Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp
 245 250 255
 Met Lys Glu Ala Leu Ile Arg Val Leu Cys Lys Lys Lys Ile Thr Phe
 260 265 270
 30 Cys Leu
 (2) INFORMATION FOR SEQ ID NO:70:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 amino acids
 (B) TYPE: amino acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
 40 Leu Ala Ile Ala Val Leu Ser Leu Thr Leu Leu Gly Thr Phe Thr Val
 1 5 10 15
 Leu Glu Asn Leu Leu Val Leu Cys Val Ile Leu His Ser Arg Ser Leu
 20 25 30
 Arg Cys Arg Pro Ser Tyr His Phe Ile Gly Ser Leu Ala Val Ala Asp
 35 40 45
 45 Leu Leu Gly Ser Val Ile Phe Val Tyr Ser Phe Val Asp Phe His Val
 50 55 60
 Phe His Arg Lys Asp Ser Pro Asn Val Phe Leu Phe Lys Leu Gly Gly
 65 70 75 80

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Val Thr Ala Ser Phe Thr Ala Ser Val Gly Ser Leu Phe Leu Thr Ala
85 90 95

Ile Asp Arg Tyr Ile Ser Ile His Pro Pro Ile Ala Tyr Lys Arg Ile
100 105 110

5 Val Arg Arg Pro Lys Ala Val Val Ala Phe Cys Leu Met Thr Ile Ala
115 120 125

Ile Val Ile Ala Val Leu Pro Leu Leu Gly Trp Asn Cys Lys Lys Leu
130 135 140

10 Gln Ser Val Cys Cys Asp Ile Phe Pro Leu Ile Asp Gly Thr Tyr Leu
145 150 155 160

Met Phe Trp Ile Gly Val Thr Ser Val Leu Leu Leu Phe Ile Val Tyr
165 170 175

Ala Tyr Met Tyr Ile Leu Trp Lys Ala His Ser His Ala Val Arg Ala
180 185 190

15 Gln Arg Gly Thr Gln Lys Ser Ile Ile Ile His Thr Ser Glu Asp Gly
195 200 205

Lys Val Gln Val Thr Arg Pro Asp Gln Ala Arg Met Asp Ile Arg Leu
210 215 220

20 Ala Lys Thr Leu Val Leu Ile Leu Val Val Leu Ile Ile Cys Trp Gly
225 230 235 240

Pro Leu Leu Ala Ile Met Val Tyr Asp Val Phe Gly Leu Leu Ile Lys
245 250 255

Thr Val Phe Ala Phe Cys Ser Leu Leu Ile Asn Ser Thr Val Asn Pro
260 265 270

25 Ile Ile Tyr Ala Leu Arg Ser Lys Asp Leu Arg His Ala Phe Arg Ser
275 280 285

Trp Pro Ser Cys Glu Gly Thr Ala Gln Pro Leu Asp Asn Ser Met Gly
290 295 300

30 Asp Ser Asp Cys Leu His Lys His Ala Asn Asn Thr Ala Ser Met His
305 310 315 320

Arg Ala Ala Glu Ser Cys Ile Lys Ser Thr Val Lys Leu Ala Leu Val
325 330 335

Ser Thr Asp Thr Ser Ala Glu Ala Leu
340 345

35 (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Lys Ala Leu Leu Ile Val Ala Tyr Ser Phe Thr Ile Val Phe Ser Leu
1 5 10 15

45 Phe Gly Asn Val Leu Val Cys His Tyr Ile Phe Lys Asn Gln Arg Lys
20 25 30

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Ile Ser Ala Thr Ser Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile
 35 40 45
 Ile Glu Thr Leu Leu Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn
 50 55 60
 5 Ser Thr Trp Tyr Phe Gly Lys Gly Met Leu His Val Ser Arg Phe Ala
 65 70 75 80
 Gln Tyr Cys Ser Leu His Val Ser Ala Leu Ile Leu Thr Ala Ile Ala
 85 90 95
 10 Val Asp Arg His Gln Val Ile Met Pro Leu Lys Pro Arg Ile Ser Ile
 100 105 110
 Thr Lys Gly Val Ile Tyr Ile Ala Val Ile Trp Val Met Thr Phe Phe
 115 120 125
 Ser Leu Pro His Ala Ile Cys Gln Lys Leu Phe Thr Phe Lys Tyr Ser
 130 135 140
 15 Glu Asp Ile Val Arg Ser Leu Cys Leu Asp Pro Phe Pro Glu Pro Ala
 145 150 155 160
 Asp Leu Phe Trp Lys Tyr Leu Asp Ile Ala Thr Phe Ile Leu Leu Tyr
 165 170 175
 20 Leu Leu Pro Leu Phe Ile Ile Ser Val Ala Tyr Ala Arg Val Ala Lys
 180 185 190
 Lys Leu Trp Leu Cys Asn Thr Ile Gly Asp Val Thr Thr Glu Gln Tyr
 195 200 205
 Leu Ala Leu Arg Arg Lys Lys Lys Thr Thr Val Lys Met Leu Val Leu
 210 215 220
 25 Val Val Val Leu Phe Ala Leu Cys Trp Phe Pro Leu Asn Cys Tyr Val
 225 230 235 240
 Leu Leu Leu Ser Ser Lys Ala Ile His Thr Asn Asn Ala Leu Tyr Phe
 245 250 255
 30 Ala Phe His Trp Phe Ala Met Ser Ser Thr Cys Tyr Asn Pro Phe Ile
 260 265 270
 Tyr Cys Trp Leu Asn Glu Asn Phe Arg Val Glu Leu Lys Ala Leu Leu
 275 280 285
 Ser Met Gln Pro Pro Pro Lys Pro Glu Asp Arg Leu Pro Ser Pro Val
 290 295 300
 35 Pro Ser Phe Arg Val Ala Trp Thr Glu Lys Ser His Gly Arg Arg Ala
 305 310 315 320
 Pro Leu Pro Asn His His Leu Pro Ser Ser Gln Ile Gln Ser Gly Lys
 325 330 335
 40 Thr Asp Leu Ser Ser Val Glu Pro Val Val Ala Met Ser
 340 345

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ile Phe Thr Ile Ala Leu Ala Tyr Gly Ala Val Ile Ile Leu Gly Val
 1 5 10 15
 Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile Leu Lys Gln Lys Glu Leu
 5 20 25 30
 Ile Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Val Trp
 35 40 45
 Leu Pro Phe Thr Phe Val Tyr Thr Leu Ile Cys His Trp Val Phe Gly
 50 55 60
 Glu Cys Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val
 10 65 70 75 80
 Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Glu Leu Ile
 85 90 95
 Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly
 15 100 105 110
 Ile Thr Val Ile Trp Val Ile Ala Val Ala Ser Ser Leu Pro Phe Val
 115 120 125
 Ile Tyr Gln Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala
 130 135 140
 Ala Phe Lys Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser
 20 145 150 155 160
 His Arg Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly
 165 170 175
 Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu
 25 180 185 190
 Lys Arg Arg Asn Asn Met Met Lys Ile Arg Asp Ser Lys Tyr Arg Ser
 195 200 205
 Ser Glu Thr Lys Arg Ile Asn Val Met Leu Leu Ser Ile Val Val Ala
 210 215 220
 Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Ile Val Phe Asp
 30 225 230 235 240
 Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu
 245 250 255
 Leu Cys His Leu Thr Leu Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
 35 260 265 270
 Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe
 275 280 285
 Cys Asp Phe Arg Ser Arg Asp Gly Arg Thr Thr Arg Leu
 290 295 300

40 (2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

	Leu	Thr	Ser	Val	Val	Phe	Ile	Leu	Ile	Cys	Cys	Phe	Ile	Ile	Leu	Glu
	1				5					10					15	
5	Asn	Ile	Phe	Val	Leu	Leu	Thr	Ile	Trp	Lys	Thr	Lys	Lys	Phe	His	Arg
				20					25					30		
	Pro	Met	Tyr	Tyr	Phe	Ile	Gly	Asn	Ile	Ala	Leu	Ser	Asp	Leu	Ile	Ala
			35					40					45			
	Gly	Val	Ala	Tyr	Thr	Ala	Asn	Leu	Leu	Leu	Ser	Gly	Ala	Thr	Thr	Tyr
		50					55					60				
10	Lys	Leu	Thr	Pro	Ala	Gln	Trp	Phe	Leu	Arg	Glu	Gly	Ser	Met	Phe	Val
	65					70					75					80
	Ala	Leu	Ser	Leu	Ser	Val	Phe	Ser	Leu	Leu	Ala	Ile	Ala	Ile	Glu	Arg
					85					90					95	
15	Tyr	Ile	Thr	Met	Leu	Lys	Met	Leu	His	Asn	Gly	Ser	Asn	Asn	Phe	Arg
				100					105					110		
	Leu	Phe	Leu	Leu	Ile	Ser	Ala	Cys	Trp	Val	Ile	Ser	Leu	Ile	Leu	Gly
			115					120					125			
	Gly	Leu	Pro	Ile	Met	Gly	Trp	Asn	Cys	Ile	Ser	Ala	Leu	Ser	Ser	Cys
		130					135					140				
20	Ser	Thr	Val	Leu	Pro	Leu	Tyr	His	Lys	His	Tyr	Ile	Leu	Phe	Cys	Thr
		145				150					155					160
	Leu	Ile	Val	Phe	Thr	Leu	Leu	Leu	Leu	Ser	Ile	Val	Ile	Leu	Tyr	Cys
					165					170					175	
25	Arg	Ile	Tyr	Ser	Leu	Val	Arg	Thr	Arg	Ser	Arg	Arg	Leu	Thr	Phe	Arg
				180					185					190		
	Lys	Asn	Ile	Ser	Lys	Ala	Ser	Arg	Ser	Ser	Glu	Asn	Val	Ala	Leu	Leu
			195					200					205			
	Lys	Thr	Val	Ile	Ile	Val	Leu	Ser	Val	Phe	Ile	Ala	Cys	Trp	Ala	Pro
		210					215					220				
30	Leu	Phe	Ile	Leu	Leu	Leu	Leu	Asp	Val	Gly	Cys	Lys	Val	Lys	Thr	Cys
	225					230					235					240
	Asp	Ile	Leu	Phe	Arg	Ala	Glu	Tyr	Phe	Leu	Val	Ile	Ala	Val	Ile	Asn
					245					250					255	
35	Ser	Gly	Thr	Asn	Pro	Ile	Ile	Tyr	Thr	Leu	Thr	Asn	Lys	Glu	Met	Arg
				260				265						270		
	Arg	Ala	Phe	Ile	Arg	Ile	Met	Cys	Cys	Lys	Cys	Pro	Ser	Gly	Asp	Ser
			275					280					285			
	Ala	Gly	Lys	Phe	Lys	Arg	Pro	Ile	Ile	Ala	Gly	Met	Glu	Phe	Ser	Arg
		290					295					300				
40	Ser	Lys	Ser	Asp	Asn	Ser	Ser	His	Pro	Gln	Lys	Asp	Glu	Gly	Asp	Asn
	305					310					315					320
	Pro	Glu	Thr	Ile	Met	Ser	Ser	Gly	Asn	Val	Asn	Ser	Ser	Ser		
					325					330						

(2) INFORMATION FOR SEQ ID NO:74:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 236 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
 Ile Thr Tyr Tyr Ile Leu Ile Gly Leu Cys Ala Val Val Gly Asn Ile
 1 5 10 15
 Leu Leu Val Ile Trp Val Val Lys Leu Asn Arg Thr Leu Arg Thr Thr
 20 25 30
 10 Thr Phe Tyr Phe Ile Val Ser Ile Ala Leu Ala Asp Ile Ala Val Leu
 35 40 45
 Val Ile Pro Leu Ala Ile Ala Ser Ala Trp Arg Ser Arg Cys Thr Ser
 50 55 60
 15 Asn Cys Leu Phe Met Ser Cys Val Leu Leu Val Phe Thr His Ala Ser
 65 70 75 80
 Ile Met Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Leu Arg Val Lys
 85 90 95
 Leu Thr Val Arg Tyr Arg Thr Val Thr Thr Gln Arg Arg Ile Trp Leu
 100 105 110
 20 Phe Leu Gly Leu Cys Trp Leu Val Ser Phe Leu Val Gly Leu Thr Pro
 115 120 125
 Trp Gly Trp Asn Arg Lys Val Thr Leu Glu Leu Ser Gln Asn Ser Ser
 130 135 140
 25 Thr Leu Arg Glu Phe Lys Thr Pro Lys Ser Leu Phe Leu Val Leu Phe
 145 150 155 160
 Leu Phe Ala Leu Cys Trp Leu Pro Leu Ser Ile Ile Asn Phe Val Ser
 165 170 175
 Tyr Phe Asn Val Lys Ile Pro Glu Thr Leu Leu Gly Ile Leu Leu Ser
 180 185 190
 30 His Ala Asn Ser Leu Pro Ile Val Tyr Ala Cys Lys Lys Lys Phe Lys
 195 200 205
 Glu Thr Tyr Phe Val Ile Leu Arg Ala Cys Arg Leu Cys Gln Thr Ser
 210 215 220
 35 Asp Ser Leu Asp Ser Asn Leu Glu Gln Thr Thr Glu
 225 230 235

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
 45 Ala Ile Leu Ile Ser Phe Ile Tyr Ser Trp Cys Leu Val Gly Leu Cys
 1 5 10 15
 Gly Asn Ser Met Val Ile Tyr Val Ile Leu Arg Tyr Ala Lys Met Lys
 20 25 30
 Thr Ala Thr Asn Ile Tyr Ile Leu Asn Ile Ala Ile Ala Asp Glu Leu

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	35	40	45
	Leu Val Pro Phe Leu Val Thr Ser Thr Leu Leu Arg His Trp Pro Phe		
	50	55	60
5	Gly Ala Leu Leu Cys Arg Leu Val Leu Ser Val Asp Ala Val Asn Met		
	65	70	75
	Phe Thr Ser Ile Tyr Cys Leu Thr Val Leu Ser Val Asp Arg Tyr Val		
		85	90
	Ala Val Val His Pro Ile Lys Ala Ala Arg Tyr Arg Arg Pro Thr Val		
		100	105
10	Ala Lys Val Val Asn Leu Gly Val Trp Val Leu Ser Leu Leu Val Ile		
		115	120
	Leu Pro Ile Trp Phe Ser Arg Thr Ala Ala Asn Ser Asp Gly Thr Val		
		130	135
15	Ala Cys Asn Met Ile Trp Glu Pro Ala Gln Phe Trp Leu Val Gly Phe		
		145	150
	Val Leu Tyr Thr Phe Leu Met Phe Leu Leu Pro Val Gly Ala Ile Cys		
		165	170
	Leu Cys Tyr Val Leu Ile Ile Ala Lys Met Arg Met Val Ala Leu Lys		
		180	185
20	Ala Gly Trp Gln Gln Arg Lys Arg Ser Glu Arg Lys Ile Thr Leu Val		
		195	200
	Met Met Val Val Met Val Phe Val Ile Cys Trp Phe Tyr Val Val Gln		
		210	215
25	Leu Val Asn Val Phe Ala Glu Gln Asp Asp Ala Thr Val Ser Gln Leu		
		225	230
	Ser Val Ile Leu Gly Tyr Ala Asn Ser Cys Ala Asn Pro Ile Leu Tyr		
		245	250
	Gly Phe Leu Ser Asp Asn Phe Lys Arg Ser Phe Gln Arg Ile Leu Cys		
		260	265
30	Leu Ser Leu Asn Ala Ala Glu Glu Pro Val Asp Tyr Tyr Ala Thr Ala		
		275	280
	Leu Lys Ser Arg Ala Tyr Ser Val Glu Asp Phe Gln Pro Glu Asn Leu		
		290	295
35	Glu Ser Gly Gly Val Phe Arg Asn Cys Thr Cys Ala Ser Arg Ile Ser		
		305	310
			315
			320
	Thr Leu		

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Val	Thr	Asn	Tyr	Ile	Phe	Leu	Leu	Leu	Cys	Leu	Cys	Gly	Leu	Val	Gly
1				5				10						15	

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Asn Gly Leu Val Leu Trp Phe Phe Gly Phe Ser Ile Lys Arg Thr Pro
 20 25 30
 Phe Ser Ile Tyr Ile Tyr Phe Leu His Ile Ala Ser Ala Asp Gly Ile
 35 40 45
 5 Tyr Leu Phe Ser Lys Ala Val Ile Ala Leu Leu Asn Met Gly Thr Phe
 50 55 60
 Leu Gly Ser Phe Pro Asp Tyr Val Arg Arg Val Ser Arg Ile Val Gly
 65 70 75 80
 10 Leu Thr Phe Phe Ala Gly Val Ser Leu Leu Pro Ala Ile Ser Ile Glu
 85 90 95
 Arg Cys Val Ser Val Ile Phe Pro Met Trp Tyr Trp Arg Arg Arg Pro
 100 105 110
 Lys Arg Leu Ser Ala Gly Val Cys Ala Leu Leu Trp Leu Leu Ser Phe
 115 120 125
 15 Leu Val Thr Ser Ile His Asn Tyr Phe Cys Leu Leu Gly His Glu Ala
 130 135 140
 Ser Gly Thr Ala Cys Leu Asn Met Asp Ile Ser Leu Leu Gly Ile Leu
 145 150 155 160
 20 Leu Phe Phe Leu Phe Cys Pro Ile Met Val Leu Pro Cys Ile Ala Leu
 165 170 175
 Leu His Val Glu Cys Arg Ala Arg Arg Gln Arg Ser Ala Lys Leu
 180 185 190
 Asn His Val Val Leu Ala Ile Val Ser Val Phe Leu Val Ser Ser Ile
 195 200 205
 25 Tyr Leu Gly Ile Asp Trp Phe Leu Phe Trp Val Phe Gln Ile Pro Ala
 210 215 220
 Pro Phe Pro Glu Tyr Val Arg Asp Leu Cys Ile Cys Ile Asn Ser Ser
 225 230 235 240
 30 Ala Lys Pro Ile Val Tyr Phe Ile Ala Gly Arg Asp Lys Ser Gln Arg
 245 250 255
 Leu Trp Glu Pro Leu Arg Val Val Phe Gln Arg Ala Leu Arg Asp Gly
 260 265 270
 Ala Glu Pro Gly Asp Ala Ala Ser Ser Thr Pro Asn Thr Val Thr Met
 275 280 285
 35 Glu Met Gln Cys Pro Ser Gly Asn Ala Ser
 290 295

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

45 Thr Thr Glu Ala Val Leu Asn Thr Phe Ile Ile Phe Val Gly Gly Pro
 1 5 10 15
 Ala Ile Val Leu Ile Thr Gln Leu Leu Thr Asn Arg Val Leu Gly Tyr

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	20	25	30
	Ser Thr Pro Thr Ile Tyr Met Arg Asn Leu Tyr Ser Thr Asn Phe Leu		
	35	40	45
5	Thr Leu Thr Val Leu Pro Phe Ile Val Leu Ser Asn Gln Trp Leu Leu		
	50	55	60
	Pro Ala Cys Tyr Val Ala Ser Cys Lys Phe Leu Ser Val Ile Tyr Tyr		
	65	70	75
	Ser Ser Cys Thr Val Gly Phe Ala Thr Val Ala Leu Ile Ala Ala Asp		
	85	90	95
10	Arg Tyr Arg Val Leu His Lys Arg Thr Tyr Ala Arg Gln Ser Tyr Arg		
	100	105	110
	Ser Leu Leu Leu Thr Trp Leu Ala Gly Leu Ile Phe Ser Val Pro Ala		
	115	120	125
15	Ala Val Tyr Thr Thr Val Val Met His His Asp Ala Asn Asp Thr Asn		
	130	135	140
	Asn Thr Asn Gly His Ala Thr Cys Val Leu Tyr Phe Val Ala Glu Glu		
	145	150	155
	Val His Thr Val Leu Leu Ser Trp Lys Val Leu Leu Thr Met Val Trp		
	165	170	175
20	Gly Ala Ala Pro Val Ile Leu Phe Tyr Ala Phe Phe Tyr Ser Thr Val		
	180	185	190
	Gln Arg Thr Ser Gln Lys Gln Arg Ser Arg Thr Leu Thr Phe Val Ser		
	195	200	205
25	Val Leu Leu Ile Ser Phe Val Ala Leu Gln Thr Pro Tyr Val Ser Leu		
	210	215	220
	Met Ile Phe Asn Ser Tyr Ala Thr Thr Ala Trp Pro Met Cys Glu His		
	225	230	235
	Leu Thr Leu Arg Arg Thr Ile Gly Thr Leu Ala Arg Val Val Pro His		
	245	250	255
30	Leu His Cys Leu Ile Asn Pro Ile Leu Tyr Ala Leu Leu Cys His Asp		
	260	265	270
	Phe Leu Gln Arg Met Arg Gln Cys Phe Arg Gly Gln Leu Ile Asp Arg		
	275	280	285
35	Ala Phe Leu Arg Ser Gln Gln Asn Gln Arg Ala		
	290	295	
(2) INFORMATION FOR SEQ ID NO:78:			
(i) SEQUENCE CHARACTERISTICS:			
(A) LENGTH: 283 amino acids			
(B) TYPE: amino acid			
40	(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear			
(ii) MOLECULE TYPE: peptide			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:			
45	Leu Gly Val Trp Leu Met Ile Val Gly Thr Phe Leu Leu Val Ile Thr		
	1	5	10
	Thr Ile Leu Tyr Tyr Arg Arg Lys Lys Lys Ser Pro Ser Asp Thr Tyr		
	20	25	30

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Ile Cys Asn Leu Ala Val Ala Asp Leu Leu Ile Val Val Gly Leu Pro
 35 40 45
 Phe Phe Leu Glu Tyr Ala Lys His His Pro Lys Leu Ser Arg Glu Val
 50 55 60
 5 Val Cys Ser Gly Leu Asn Ala Cys Phe Tyr Ile Cys Leu Phe Ala Gly
 65 70 75 80
 Val Cys Phe Leu Ile Asn Leu Ser Met Asp Arg Tyr Cys Val Ile Val
 85 90 95
 10 Trp Gly Val Glu Leu Asn Arg Val Arg Asn Asn Lys Arg Ala Thr Cys
 100 105 110
 Trp Val Val Ile Phe Trp Ile Ile Ala Val Leu Met Gly Met Pro His
 115 120 125
 Tyr Ile Met Tyr Ser His Thr Asn Asn Glu Cys Val Gly Trp Phe Ala
 130 135 140
 15 Asn Glu Thr Ser Cys Trp Phe Pro Val Phe Leu Asn Thr Lys Val Asn
 145 150 155 160
 Ile Cys Gly Tyr Leu Ala Pro Ile Ala Leu Met Ala Tyr Tyr Asn Arg
 165 170 175
 20 Met Val Arg Phe Ile Ile Asn Tyr Val Gly Lys Trp Phe Met Gln Thr
 180 185 190
 Leu His Val Leu Leu Val Val Val Val Ser Phe Ala Ser Phe Trp Phe
 195 200 205
 Pro Phe Asn Leu Ala Leu Phe Leu Glu Ser Ile Arg Leu Ile Ala Gly
 210 215 220
 25 Val Tyr Asn Asp Thr Leu Gln Asn Val Ile Ile Phe Cys Leu Tyr Val
 225 230 235 240
 Gly Gln Phe Ile Ala Tyr Val Arg Ala Cys Leu Asn Pro Gly Ile Tyr
 245 250 255
 30 Ile Leu Val Cys Thr Trp Phe Leu Arg Val Phe Ala Cys Cys Cys Val
 260 265 270
 Lys Gln Glu Ile Pro Tyr Gln Asp Ile Asp Ile
 275 280

(2) INFORMATION FOR SEQ ID NO:79:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:
 Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser Ile
 1 5 10 15
 Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile Gln
 20 25 30
 45 Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu Leu
 35 40 45
 Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His Asn

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	50		55		60											
	Ser 65	Leu	Ala	Ser 70	Leu	Ile	Pro	Cys	Thr	Leu 75	Leu	Thr	Ala	Cys	Phe	Tyr 80
5	Val	Ala	Ile	Thr 85	Ala	Ser	Leu	Cys	Phe	Ile 90	Thr	Glu	Ile	Ala	Leu 95	Ile
	Asp	Arg	Tyr	Tyr 100	Ala	Ile	Val	Tyr	Met	Arg 105	Tyr	Arg	Pro	Val	Lys	Ile
	Gln	Ala	Cys	Leu 115	Phe	Ser	Ile	Phe	Trp	Trp 120	Ile	Phe	Ala	Val	Ile	Ile
10	Ala	Ile	Pro	His	Phe	Met	Val	Val	Ile	Thr	Lys	Lys	Asp	Asn	Gln	Cys
	Met	Thr	Asp	Tyr	Asp	Tyr	Leu	Glu	Val	Ser	Tyr	Pro	Ile	Ile	Leu	Asn
	Val	Glu	Leu	Met	Leu	Gly	Ala	Phe	Val	Ile	Pro	Leu	Ser	Val	Ile	Ser
15	Tyr	Cys	Tyr	Tyr 180	Arg	Ile	Ser	Arg	Ile	Val	Ala	Val	Ser	Gln	Ser	Arg
	His	Lys	Gly	Arg	Ile	Val	Arg	Val	Leu	Ile	Ala	Trp	Leu	Val	Phe	Ile
	Ile	Phe	Trp	Leu	Pro	Tyr	His	Leu	Thr	Leu	Phe	Val	Asp	Thr	Ile	Ile
20	Lys	Leu	Leu	Lys	Trp	Ile	Ser	Ser	Ser	Cys	Glu	Phe	Glu	Arg	Ser	Leu
	Lys	Arg	Ala	Leu	Ile	Leu	Thr	Glu	Ser	Leu	Ala	Phe	Cys	His	Cys	Cys
25	Leu	Asn	Pro	Leu	Leu	Tyr	Val	Phe	Val	Ile	Gly	Thr	Lys	Phe	Arg	Lys
	Asn	Tyr	Thr	Val	Cys	Trp	Pro	Ser	Phe	Ala	Ser	Asp	Ser	Phe	Pro	Ala
30	Met	Tyr	Pro	Gly	Thr	Arg	Ala									

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

40	Asp	Asp	Asp	Asp	Asn	Ile	Trp	Ser	Ile	Phe	Asp	Trp	Ile	Gly	Tyr	Leu
	1				5					10					15	

	Asn	Ser	Ile	Ser	Met	Val	Ile	Tyr	Thr	Leu	Phe	Lys	Lys	Lys	Lys
				20					25					30	

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
Asp Asp Asp Asp Asn Ile Trp Asn Ile Phe Ser Thr Ile Gly Tyr Leu
1 5 10 15
Asn Ser Ile Ser Pro Val Ser Val Ile Met His Ile Tyr Gly Lys Lys
20 25 30
Lys Lys

(2) INFORMATION FOR SEQ ID NO:82:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
Asp Asp Asp Asp Gly Tyr Ser Ile Tyr Asp Thr Leu Val Thr Phe Ala
1 5 10 15
Ile Asn Pro Val Tyr Ile Thr Val Phe Lys Lys Lys Lys
20 25

(2) INFORMATION FOR SEQ ID NO:83:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
Asp Asp Asp Asp Asn Ala Trp Ser Ala Phe Asp Trp Ala Leu Tyr Leu
1 5 10 15
Asn Ser Ile Ser Met Ala Ile Tyr Thr Tyr Ala Lys Lys Lys Lys
20 25 30

(2) INFORMATION FOR SEQ ID NO:84:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
Leu Phe Ser Phe Ile Thr Trp Leu Gly Tyr Ala Asn Ser Ser Leu Asn
1 5 10 15
Pro Ile Ile Tyr Thr Thr Phe
20

(2) INFORMATION FOR SEQ ID NO:85:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:
Tyr Thr Ile Tyr Ser Ser Ser Val Val Phe Phe Ala Pro Ser Leu Ala
1 5 10 15
Ile Met Val Ile Thr Tyr Thr
20

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(2) INFORMATION FOR SEQ ID NO:86:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
 Ile Trp Leu Thr Ser Asp Ile Met Ser Thr Ser Ser Ile Leu His Asn
 1 5 10 15
 Leu Cys Val Ile Ser Phe
 20

(2) INFORMATION FOR SEQ ID NO:87:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:
 Ile Trp Ser Ile Phe Ser Ser Asp Ile Val Val Gly Tyr Ala Asn His
 1 5 10 15
 Ser Ser Leu Ala Ile Met Cys Pro Ile Val Ile Tyr Thr Val
 20 25 30

(2) INFORMATION FOR SEQ ID NO:88:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:
 Ile Phe Thr Ile Phe Ser Ser Asp Ile Ala Val Gly Tyr Ala Asn His
 1 5 10 15
 Ser Ser Ala Ala Ile Met Pro Ile Val Ile Tyr Ser Val
 20 25

(2) INFORMATION FOR SEQ ID NO:89:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:
 Lys Asn Ala Ser Ala Leu Leu Ser Val Ile Ile Ile Asn Ser Ile Gly
 1 5 10 15
 Gly Asn Val Val Thr Ala Val Ser
 20

(2) INFORMATION FOR SEQ ID NO:90:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:
 Tyr Phe Leu Met Ser Leu Ala Val Thr Asp Leu Val Val Ser Phe Val
 1 5 10 15

- 137 -

Met Pro Val Ser Ala Leu
20

(2) INFORMATION FOR SEQ ID NO:91:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ala Ile Thr Lys Ile Ala Ile Thr Trp Ala Ile Ser Gly Val Ser Val
1 5 10 15

Pro Phe Ile Pro Val Trp Gly
20

15 (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Leu Gly Ile Ile Phe Gly Thr Phe Ile Ile Trp Leu Pro Phe Phe
1 5 10 15

25 Ile Thr Asn Leu Val Ser Pro Ile
20

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
30 (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

35 Ile Trp Ile Ser Leu Asp Val Leu Phe Ser Thr Ala Ser Ser Ile Met
1 5 10 15

His Leu Cys Ala Ile Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:94:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Gly Tyr Thr Ile Tyr Ser Thr Leu Val Thr Phe Tyr Ile Pro Ser Val
1 5 10 15

Ile Met Val Ile Thr Tyr Gly
20

50

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
55 (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

- 138 -

Leu Leu Asn Phe Phe Asn Trp Ile Gly Tyr Leu Asn Ser Leu Ile Asn
1 5 10 15
Pro Val Ile Tyr Thr Leu Phe
20

WHAT IS CLAIMED IS:

1. A G-protein coupled receptor polypeptide, consisting essentially of an amino acid sequence of 15 to 40 amino acids substantially corresponding to a fragment or consensus peptide of a transmembrane domain of a G-protein coupled receptor, wherein said polypeptide has a GPR-related biological activity selected from binding a GPR ligand or modulating GPR ligand binding to a GPR.
2. A polypeptide according to claim 1, wherein said polypeptide is selected from a synthetic polypeptide, a recombinant polypeptide or a purified polypeptide.
3. A polypeptide according to claim 1, wherein said G-protein coupled receptor is a receptor selected from a cAMP receptor, an adenosine receptor, a β -adrenergic receptor, a muscarinic acetylcholine receptor, an α -adrenergic receptor, a serotonin receptor, a histamine H2 receptor, a thrombin receptor, a kinin receptor, a follicle stimulating hormone receptor, an opsin, a rhodopsin, an odorant receptor, a cytomegalovirus receptor, or a *mas* oncogene GPR.
4. A polypeptide according to claim 1, wherein said transmembrane domain is selected from at least one of transmembrane domain TM1, TM2, TM3, TM4, TM5, TM6 or TM7.
5. A polypeptide according to claim 3, wherein said transmembrane domain is a D₂ receptor transmembrane segment III or segment V.
6. A polypeptide according to claim 4, wherein said polypeptide has the amino acid sequence of Fig. 2 (SEQ ID NO:2).
7. A polypeptide according to claim 4, wherein said polypeptide has the amino acid sequence of Fig. 3 (SEQ ID NO:3).
8. A polypeptide according to claim 4, wherein said polypeptide has an amino acid sequence selected from one of SEQ ID NOS:80-95.
9. A polypeptide according to claim 4, wherein said polypeptide has an amino acid sequence of one of SEQ ID NOS:96-348.
10. A polypeptide according to claim 9, wherein said polypeptide has an amino acid sequence from one of SEQ ID NOS:96-225.

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11. A polypeptide according to claim 9, wherein said polypeptide has an amino acid sequence from one of SEQ ID NOS:226-289.

12. A polypeptide according to claim 9, wherein said
5 polypeptide has an amino acid sequence from one of SEQ ID NOS:290-297.

13. A polypeptide according to claim 9, wherein said polypeptide has an amino acid sequence from one of SEQ ID NOS:298-324.

10 14. A polypeptide according to claim 9, wherein said polypeptide has an amino acid sequence from one of SEQ ID NOS:325-338.

15 15. A polypeptide according to claim 9, wherein said polypeptide has an amino acid sequence from one of SEQ ID NOS:339-348.

16. A polypeptide according to claim 3, wherein said transmembrane domain is a dopamine receptor transmembrane domain selected from the group consisting of a D₁, D₂, D₃, D₄ or D₅ transmembrane domain.

20 17. A composition comprising a polypeptide according to claim 1, or a pharmaceutically acceptable ester, ether, sulfate, carbonate, glucuronide or salt thereof, and a pharmaceutically acceptable carrier.

25 18. A composition according to claim 16, wherein said transmembrane domain is D₂ receptor transmembrane segment III or segment V.

30 19. A composition according to claim 18, further comprising a drug selected from a phenothiazine derivative, a thioxanthine derivative, a butyrophenone derivative, a dihydroindolone, a dibenzoxazepine derivative and an atypical neuroleptic.

35 20. A method for treating a subject suffering from a pathology related to an abnormality of a G-protein coupled receptor, comprising administering to said subject a therapeutically effective amount of composition according to claim 16.

21. The method of claim 20, wherein said pathology is a psychotic disorder.

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22. The method of claim 21, wherein said psychotic disorder is a schizophrenia.

23. The method of claim 20, wherein said composition is administered to provide said polypeptide, fragment or consensus peptide thereof, in an amount ranging from about 0.01 μ g to 100 mg/kg per day.

24. The method of claim 23, wherein said composition is administered to provide said polypeptide, fragment or consensus peptide thereof, in an amount ranging from about 10 μ g to 10 mg/kg per day.

25. The method of claim 20, wherein said administering is by oral, mucosal, intravenous, intramuscular or parenteral administration.

26. A method for producing a polypeptide according to claim 1, wherein said polypeptide is a recombinant polypeptide obtained from a recombinant host which expresses a heterologous nucleic acid encoding said polypeptide, comprising the steps of:

(A) providing a host comprising a recombinant nucleic acid encoding a polypeptide according to claim 1 in expressible form;

(B) culturing said host under conditions such that said polypeptide is expressed in recoverable amounts; and

(C) recovering said polypeptide produced by said host.

27. The method of claim 26, further comprising:

(D) purifying said polypeptide.

28. The method of claim 26, wherein said host is a bacteria or a eukaryotic cell.

29. The method of claim 28, wherein said eukaryotic cell is a mammalian cell, an insect cell or a yeast cell.

30. A method for producing a polypeptide according to claim 1, comprising:

(A) chemically synthesizing a polypeptide according to claim 1 in recoverable amounts; and

(B) recovering said polypeptide.

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31. A method for isolating a G-protein coupled receptor, fragment or consensus sequence thereof, or a protein that binds the G-protein coupled receptor, comprising

5 (A) providing a bound support, said support being bound to a polypeptide according to claim 1, or an antibody, anti-idiotypic antibody, or a fragment thereof;

(B) contacting a sample containing said G-protein coupled receptor or said protein that binds a G-protein coupled receptor to said bound support, such that said
10 receptor or protein is reversibly bound to said bound support; and

(C) recovering said receptor or protein that is attached to the bound support by dissociating the receptor or protein under conditions that cause elution or
15 dissociation of the receptor or protein from said bound support.

32. A method according to claim 31, wherein said GPR is a dopamine receptor.

33. An antibody, anti-idiotypic antibody or a fragment of
20 said antibody or anti-idiotypic antibody, that specifically displays an epitope of a G-protein coupled receptor polypeptide, according to claim 1.

34. A recombinant nucleic acid comprising a nucleotide sequence encoding a G-protein coupled receptor polypeptide according
25 to claim 1.

35. A vector comprising a nucleic acid according to claim 34.

36. A host cell comprising the nucleic acid of claim 34.

37. A host cell according to claim 36, wherein said host
30 cell is selected from a mammalian cell, a yeast cell, a bird cell or an insect cell.

38. A host cell according to claim 36, wherein, when said nucleic acid is expressed as said receptor polypeptide in said host cell, a receptor binding molecule comprising said env binding domain
35 binds to said receptor polypeptide.

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39. A host cell according to claim 37, wherein said host cell is a mammalian cell selected from a human cell, a primate cell or a rodent cell.

40. A method for isolating a protein that binds a
5 G-protein coupled receptor, comprising

(A) providing a bound support, said support being bound to a polypeptide according to claim 1, or anti-idiotypic antibody thereto;

10 (B) contacting a sample containing said protein that binds a G-protein coupled receptor to said bound support, such that said protein is reversibly bound to said bound support; and

15 (C) recovering said protein that is attached to the bound support by dissociating the receptor or protein under conditions that cause elution or dissociation of the protein from said bound support.

41. A method according to claim 40, wherein said GPR is a dopamine receptor.

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LSLLLSLLSLLLSLLSLLLSLYYY

FIGURE 1

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DDIFVTLDVLFSTASILNLSAISLKKK

FIGURE 2

DYAI FVLYASAWLS FNCPFIVTLNIK

FIGURE 3

KAVVYSSIVSFFYVFD

FIGURE 4

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DCDVVFVVDIMLCT^{ASIFNLCAISVGK}

FIGURE 5

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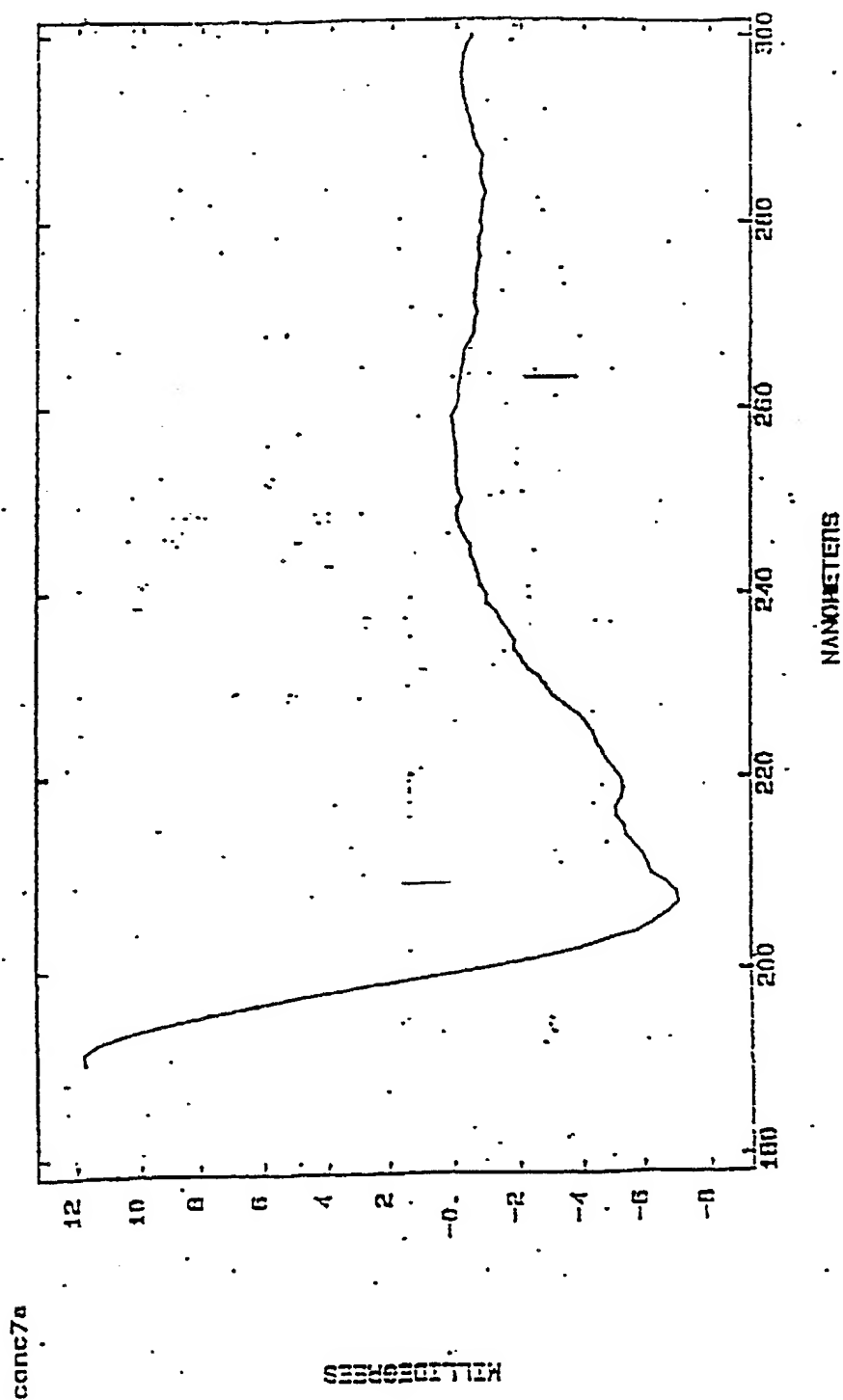


FIG. 6

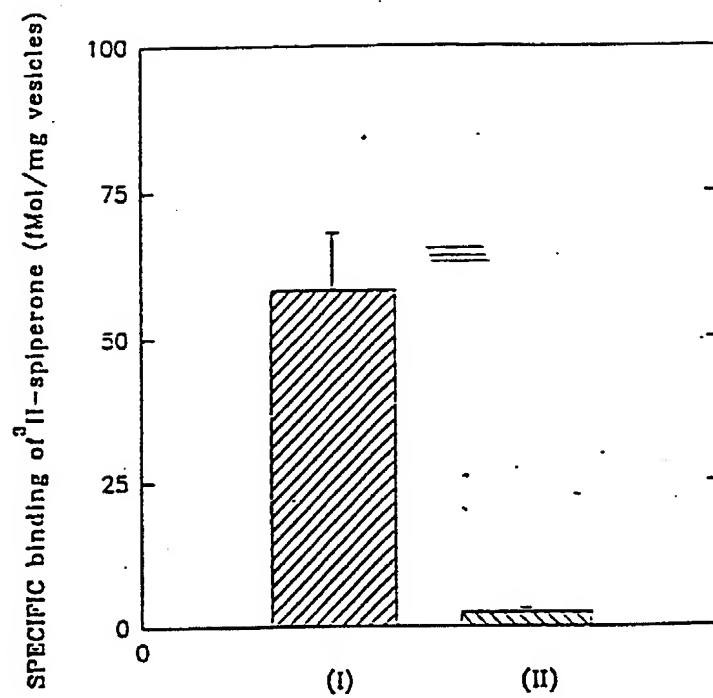


FIGURE 7

1. Dictyostellium cAMP receptor (Klein et al., 1988)
2. Dog Adenosine A2 receptor (RDC3) (Libert et al., 1989b)
3. Dog Adenosine A1 receptor (RDC7) (Libert et al., 1989b)
4. Human m1 muscarinic acetylcholine receptor (Peralta et al., 1987)
5. Human m2 muscarinic acetylcholine receptor (Peralta et al., 1987)
6. Human m3 muscarinic acetylcholine receptor (Peralta et al., 1987)
7. Human m4 muscarinic acetylcholine receptor (Peralta et al., 1987)
8. Human m5 muscarinic acetylcholine receptor (Bonner et al., 1988)
9. Human beta 1 adrenergic receptor (Friedle et al., 1987)
10. Human beta 2 adrenergic receptor (Kobilka et al., 1987a)
11. Human beta 3 adrenergic receptor (Kobayashi et al., 1989)
12. Cow alpha 1 adrenergic receptor (Schwinn et al., 1990)
13. Rat alpha 1B adrenergic receptor (Voigt, et al., 1990)
14. Human alpha 2 C1 adrenergic receptor (Ragan et al., 1988)
15. Human alpha 2 C2 adrenergic receptor (Lomasney et al., 1990)
16. Human alpha 2 C10 adrenergic receptor (Kobilka et al., 1987c)
17. Rat alpha 2 adrenergic receptor R20 (Hanler et al., 1991)
18. Drosophila octopamine receptor (Arakawa et al., 1990)
19. Human dopamine D1 receptor (Deary et al., 1990)
20. Human dopamine D3 receptor (Sunahara et al., 1991)
21. Human dopamine D2 receptor (Grandy et al., 1989)
22. Human dopamine D3 receptor (Giras et al., 1990)
23. Human dopamine D4 receptor (Van Tol et al., 1991)
24. Human serotonin 1d receptor (RDC4) (Hambin and Metcalfe, 1991)
25. Human serotonin 1a receptor (Kobilka et al., 1987b)
26. Rat serotonin 1c receptor (Julius et al., 1988)
27. Rat serotonin 2 receptor (Julius et al., 1990)
28. Human histamine H2 receptor (Gantz et al., 1991)
29. Human N-formyl peptide receptor (Boulay et al., 1990)
30. Human C5a anaphylatoxin receptor (Garard and Gerard, 1991)
31. Human thrombin receptor (Vu et al., 1991)
32. Human thrombosane A2 receptor (Miyata et al., 1991)
33. Human IL-8 receptor (Murphy and Tiffany, 1991)
34. Guinea-pig platelet-activating factor receptor (Honda et al., 1991)
35. Cow endothelin 1 receptor (Arai et al., 1990)
36. Rat non-isopeptide selective endothelin receptor (Sakurai et al., 1990)
37. Mouse bombesin/gastrin releasing peptide receptor (Spindel et al., 1991)
38. Rat neuropeptide Y preferring bombesin receptor (Mada et al., 1991)
39. Human vasoactive intestinal peptide (Sreedharan et al., 1991)
40. Rat neuropeptide Y receptor (Tanaka et al., 1990)
41. Rat bradykinin receptor (Gschlatter et al., 1991)
42. Mouse thyrotropin-releasing hormone receptor (Straub et al., 1990)
43. Human neurokinin A (NK) receptor (Gerard et al., 1990)
44. Rat substance P receptor (Yokota et al., 1989)
45. Rat neuropeptide K receptor (Shigemoto et al., 1990)
46. Bovine adrenal angiotensin II type-1 receptor (Sasaki et al., 1991)
47. Human mas oncogene (angiotensin) receptor (Young et al., 1986)
48. Human lutropin-choriogonadotropin receptor (Frazier et al., 1990)
49. Human thyrotropin receptor (Libert et al., 1989a)
50. Human follicle stimulating hormone receptor (Miyagishi et al., 1991)
51. Human rhodopsin (Mathias and Strydom, 1984)
52. Human green opsin (Mathias et al., 1986)
53. Human red opsin (Mathias et al., 1986)
54. Human blue opsin (Mathias et al., 1986)
55. Odorant receptor F3 (Buck and Axel, 1991)
56. Odorant receptor F5 (Buck and Axel, 1991)
57. Odorant receptor F6 (Buck and Axel, 1991)
58. Odorant receptor F12 (Buck and Axel, 1991)
59. Odorant receptor I3 (Buck and Axel, 1991)
60. Odorant receptor I7 (Buck and Axel, 1991)
61. Odorant receptor I8 (Buck and Axel, 1991)
62. Odorant receptor I9 (Buck and Axel, 1991)
63. Odorant receptor I14 (Buck and Axel, 1991)
64. Odorant receptor I15 (Buck and Axel, 1991)
65. Human cannabinoid receptor (Matsuda et al., 1990)
66. Mouse glucocorticoid-induced receptor (Harrison et al., 1991)
67. Rat FCR (Eva et al., 1990)
68. Human endothelial cell GPR OLA and Mac1a, 1990)
69. Rat vasist G-protein coupled receptor 1 (Meyerhof et al., 1991a)
70. Rat RGM7 (Meyerhof, DNA and Cell Biology, in press, 1991b)
71. Human thoracic aorta GPR (Ross et al., 1990)
72. Cytomegalovirus (Human) GPR, US13 (Chee et al., 1990)
73. Cytomegalovirus (Human) GPR, US17 (Chee et al., 1990)
74. Cytomegalovirus (Human) GPR, US18 (Chee et al., 1990)

FIGURE 8A

1 MLLDGNFANE
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73 MLLDGNFANE
74 MLLDGNFANE

FIGURE 8B

[illegible]

FIGURE 8C

6

1	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
2	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
3	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
4	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
5	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LALVGLFALCPLVHINCTTY	CPSKSHAP
6	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
7	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
8	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
9	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
10	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
11	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
12	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
13	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
14	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
15	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
16	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
17	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
18	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
19	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
20	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
21	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
22	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
23	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
24	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
25	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
26	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
27	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
28	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
29	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
30	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
31	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
32	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
33	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
34	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
35	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
36	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
37	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
38	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
39	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
40	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
41	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
42	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
43	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
44	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
45	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
46	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
47	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
48	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
49	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
50	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
51	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
52	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
53	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
54	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
55	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
56	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
57	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
58	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
59	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
60	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
61	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
62	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
63	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
64	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
65	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
66	KEKCAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP
67	(83) - KCKPRCKECLAKKCTSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
68	(110) - K-LVCKX-CPAKOP-PPSREKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
69	(166) - KRFALKRSCTVURRSVVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
70	(113) - K-FASLAKCVROCKN-AARERKVTCT	LSAFLAFITLMTFNDVWSTF	COCVPE
71	(155) - K-LNPNFSSHCKGCKSVKCKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
72	AAAAATAPLAKGRACKRPSVAVLRECKAART	LSAFLAFITLMTFNDVWSTF	COCVPE
73	KEKLTTCFK	LENTTFFVLCVAVVWVWV	NFTPALNLTCT
74	KEVHAAS	LALVGLFALCPLVHINCTTY	CPSKSHAP

FIGURE 8F

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1 SVSHGTWASVITINPFI-YATF CAXILTVITITGTVGVOKLEKXNNNPSPYSSSRGTSCD-GCHFTEDVOCSSDMECCSLEHNPW- (63)
 2 LMTLTVLSHNSVNPFI-YATF IREFAGTFRKILSHVLRREPFRAGTSARALAAHSGDZQSLRNGHPGVWANGSAPHENRPNCT- (50)
 3 LMTLTVLSHNSVNPFI-YATF IQKFRVITLKTANDHFRQPIPVODPPLEAPHD

4 LDELGTWLTINSTNPI-YALC NKAFROTFRLLCGRKRWKIPKPCSVHRTPSRQC
 5 VMTGTWLTINSTNPI-YALC NATFKOTFRLLCGRKRWKIPKPCSVHRTPSRQC
 6 VMTGTWLTINSTNPI-YALC NKIFRTFRLLCGRKRWKIPKPCSVHRTPSRQC
 7 VMTGTWLTINSTNPI-YALC NATFKOTFRLLCGRKRWKIPKPCSVHRTPSRQC
 8 LDELGTWLTINSTNPI-YALC NKIFRTFRLLCGRKRWKIPKPCSVHRTPSRQC

9 LFTVMTGYSANPFI-YCRS PDFRAFGTLLCGRKRWKIPKPCSVHRTPSRQC (25)
 10 VMTGTWLTINSTNPI-YCRS PDFRAFGTLLCGRKRWKIPKPCSVHRTPSRQC (23)
 11 AFLAHLWLTINSTNPI-YCRS PDFRAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 12 VMTGTWLTINSTNPI-YCRS SQEFKAFQWLTINSTNPI-YCRS SHVLEGGQOLVRIPOVSAETTYKSKDQVCEKCT- (66)
 13 VMTGTWLTINSTNPI-YCRS SKELFRAFGTLLCGRKRWKIPKPCSVHRTPSRQC (93)
 14 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 15 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 16 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 17 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 18 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 19 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 20 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 21 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 22 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 23 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 24 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 25 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 26 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 27 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 28 LFTVMTGYSANPFI-YCRS NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC

29 AVDTSLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 30 LFTVMTGYSANPFI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 31 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 32 LFTVMTGYSANPFI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 33 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 34 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 35 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 36 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 37 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 38 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 39 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 40 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 41 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 42 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 43 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 44 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 45 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 46 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 47 AYLLAFTNPI-YVTH GDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC

48 VLLVFTPI-YATF NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 49 VLLVFTPI-YATF NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 50 VLLVFTPI-YATF NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC

51 DFTVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 52 DFTVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 53 DFTVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 54 DFTVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC

55 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 56 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 57 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 58 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 59 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 60 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 61 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 62 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 63 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC
 64 --EASVMTGYSANPFI-YVTH NKDFRFGTLLCGRKRWKIPKPCSVHRTPSRQC

65 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 66 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 67 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 68 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 69 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 70 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 71 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 72 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 73 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC
 74 VFAFGTLLCGRKRWKIPKPCSVHRTPSRQC

FIGURE 8G

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/08528

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) : C07K 7/00, 15/06; C12N 15/12

US CL : 435/69.1; 514/12, 13, 14, 15, 16, 17; 530/387.9

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1; 514/12, 13, 14, 15, 16, 17; 530/387.9

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN/MEDLINE

search terms: G protein coupled, receptor#, fragment#

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	NATURE, Vol. 336, issued 22 December 1988, J. R. Bunzow et.al., "Cloning and expression of a rat D2 dopamine receptor cDNA", pages 783-787. See entire document.	1-41
A	Biochemistry, Vol. 26, No. 10, issued 19 May 1987, H. G. Dohlman et.al., "A Family of Receptors Coupled to Guanine Nucleotide Regulatory Proteins", pages 2657-2664. See entire document.	1-41
A	BIO/TECHNOLOGY, Vol. 7, issued September 1989, S. Marullo et.al., "EXPRESSION OF HUMAN B1 AND B2 ADRENERGIC RECEPTORS IN E. COLI AS A NEW TOOL FOR LIGAND SCREENING", pages 923-927. See entire document.	1-41

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

25 October 1993

Date of mailing of the international search report

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